

Appendix

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SUPPLEMENTARY TABLES

Table S1. Parameter values and sources

| Parameter | Description | Value / distribution | Source |
|---|---|---------------------------------------|--|
| Parameters relating to the SARS-CoV-2 infection process | | | |
| $1/\varepsilon$ | Duration of latent period (days) | $\sim \text{Gamma}(\mu = 2.5, k = 4)$ | Incubation period (latent period plus duration of preclinical infection) of mean 5 days ¹ subdivided into latent period (mean 2.5) and preclinical infection (mean 2.5 days). |
| $1/\tau$ or $d_{\text{preclinical_infection}}$ | Duration of preclinical infection (days) | $\sim \text{Gamma}(\mu = 2.5, k = 4)$ | Incubation period (latent period plus duration of preclinical infection) of mean 5 days ¹ subdivided into latent period (mean 2.5) and preclinical infection (mean 2.5 days). |
| $d_{\text{clinical_infection}}$ ($1/\omega + 1/\varphi$) | Duration of clinical infection (symptomatic disease) (days) | $\sim \text{Gamma}(\mu = 5, k = 4)$ | Assumed duration of clinical infection of mean 5 days (approximated from ²⁻⁴), subdivided into highly infectious clinical infection and less infectious clinical infection, corresponding to a linear decrease in viral load. ² |
| $1/\omega$ or $d_{\text{clinical_infection_h}}$ | Duration of early highly infectious stage of clinical infection (days) | $d_{\text{clinical_infection}}/2$ | |
| $1/\varphi$ or $d_{\text{clinical_infection_l}}$ | Duration of late low infectious stage of clinical infection (days) | $d_{\text{clinical_infection}}/2$ | |
| $d_{\text{total_infectiousness}}$ or $d_{\text{asymptomatic_infection}}$ or $1/\varphi_a$ | Total duration of infectiousness or duration of asymptomatic infection (days) | $1/\tau + 1/\omega + 1/\varphi$ | |

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| $R0_a$ | R0 in the care home for pathway (a), ie. the transmission pathway in which individuals (eventually) present with symptoms | Baseline: ~ $Gamma(\mu = 2, k = 8)$ | Assumed (baseline). |
| $p_{transmission_{pc_vs_c}}$ | Probability that transmission in pathway (a) occurs during the preclinical stage compared to the clinical stages | ~ $Beta(\mu = 0.4, se = 0.05)$ | Pre-clinical stage on average 40% of transmission compared to clinical stage. ^{2,3} |
| $p_{transmission_{cl_vs_ch}}$ | Probability that transmission during the clinical stages occurs during the late low infectiousness stage (a) compared to the early high infectiousness stage | ~ $Beta(\mu = 0.3, se = 0.05)$ | We assumed a linear decrease in viral load over the symptomatic period. ² |
| m_{R0_b} | Relative R0 pathway (b) vs pathway (a) | ~ $Beta(\mu = 0.5, se = 0.1)$ | We assumed the relative infectiousness of pathway (b) was on average half of that of (a). ⁵ |
| $m\beta_d$ | Relative transmission rates in care home when an infected resident/staff member is detected (ie. ≥ 1 resident isolated or staff member absent) vs not | Baseline: ~ $Gamma(\mu = 0.5, k = 15)$ | Assumed (baseline). |
| m_i | Relative infectiousness of residents being isolated vs not | ~ $Beta(\mu = 0.25, se = 0.1)$ | Assumed (baseline). |
| n_V | Number of visitors per resident in the care home on any one day | Baseline: ~ $Beta(\mu = 0.24, se = 0.1)$ | Baseline: Expert opinion (Chair of the Centre for Policy on Ageing and was Executive Director of |

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| | | | the National Care Forum from 2003 to 2016, founder-Chair of the Care Provider Alliance, D Kelly, personal communication, March 2020)(“around 10% don't have any and 10% have visitors every day. Of the remaining 80% I reckon they could be divided between half having a couple of visitors a week and half 1 visitor every 2 weeks”). (0.1*1)+(0.4*(2/7))+(0.4*(1/14))= 0.24 |
| $p_{v_{infectious}}$ | Probability of a visitor being infectious with SARS-CoV-2 | Baseline (medium community prevalence scenario): $\sim Gamma(\mu = 0.002, k = 20)$; low community prevalence scenario: $\sim Gamma(\mu = 0.0004, k = 20)$ high community prevalence scenario: $\sim Gamma(\mu = 0.01, k = 20)$ | Median of 500 runs $p(\text{infected with preclinical infection}) + p(\text{infected asymptomatic})$ in England from Davies et al. 2020 model ⁵ on 2020-09-30 (baseline, medium community prevalence scenario), 2020-07-15 (low community prevalence scenario) or 2020-04-01 (high community prevalence scenario). |
| p_a | Probability an exposed resident becomes asymptomatic | $\sim Beta(\mu = 0.4, se = 0.1)$ | The proportion of infected residents with asymptomatic infection ranged from 6-45% in the literature. ⁶⁻¹¹ |
| p_{as} | Probability an exposed staff member becomes asymptomatic | $\sim Beta(\mu = 0.5, se = 0.05)$ | Assumed. ⁵ |
| R_c | Reproduction number in the community | Baseline (medium community prevalence scenario): $\sim Gamma(\mu = 1, k = 16)$; low | Assumed. |

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| | | community prevalence scenario: ~ $\text{Gamma}(\mu = 0.8, k = 16)$; high community prevalence scenario: ~ $\text{Gamma}(\mu = 1.5, k = 16)$ | |
| $d_{\text{total_infectiousness_C}}$ | Duration of infectiousness in the community (days) | ~ $\text{Gamma}(\mu = 5, k = 4)$ | Assumed 5 days. ⁵ |
| $p_{c_{\text{infectious}}}$ | Probability of a community member being infectious with SARS-CoV-2 | Baseline (medium community prevalence scenario): ~ $\text{Gamma}(\mu = 0.003, k = 20)$; low community prevalence scenario: ~ $\text{Gamma}(\mu = 0.0005, k = 20)$; high community prevalence scenario: ~ $\text{Gamma}(\mu = 0.01, k = 20)$; | Median of 500 runs $p(\text{infected with preclinical infection}) + p(\text{infected asymptomatic}) + p(\text{infected clinical infection})$ in England from Davies et al. 2020 model ⁵ on the 2020-09-30 (baseline, medium community prevalence scenario), 2020-07-15 (low community prevalence scenario) or 2020-04-01 (high community prevalence scenario). |
| $p_{\text{original staff work at care home 2}}$ | Probability of original staff working at another care home | ~ $\text{Beta}(\mu = 0.01, se = 0.005)$ | C Watson (lead of care home survey Thames Valley), personal communication, June 2020. |
| $p_{\text{replacement staff work at care home 2}}$ | Probability of replacement staff working at another care home | ~ $\text{Beta}(\mu = 0.2, se = 0.0)$ | Assumed. |
| $p_{\text{care home outbreak}}$ | Probability that another care home is experiencing an outbreak | Baseline (medium community prevalence scenario): ~ $\text{Beta}(\mu = 0.25, se = 0.0)$; low community prevalence scenario :~ | Assuming 25% of care homes have an ongoing outbreak, i.e. ~4,000 of 15,000 care homes in baseline scenario (unpublished data, Public Health England). In the high |

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| | | $Beta(\mu = 0.1, se = 0.0)$; high community prevalence scenario : $\sim Beta(\mu = 0.4, se = 0.0)$ | community prevalence scenario we assumed 40% of care homes could have an outbreak and in the low community prevalence scenario, 10%. |
| $p_{res\ inf}$ or $p_{staff\ inf}$ | Probability that a resident in a care home with an outbreak is infectious or probability that a staff member in a care home with an outbreak is infectious | $\sim Beta(\mu = 0.1, se = 0.0)$ | Corresponds to approximately 3 residents or staff in an average residential care home being infectious. |
| $1/v$ | Duration of staff absence (days) | $\sim Gamma(\mu = 14, k = 40)$ | Assuming staff absent for 14 days. |
| Parameters relating to flows in and out of the care home | | | |
| δ | Death rate pppd in the care home for residents without COVID-19 clinical infection | $\sim Gamma(\mu = 0.0005, k = 12)$ for residential care homes and $\sim Gamma(\mu = 0.001, k = 12)$ for nursing care homes | See Supplementary material A1. |
| CFR | Case fatality ratio in residents | $\sim Beta(\mu = 0.25, se = 0.0)$ | Literature estimates range from 17-36% ^{6-9,12,13} |
| $p_{death\ res\ within\ care\ home}$ | Probability resident with COVID-19 dies within the care home (vs. hospital) | $\sim Beta(\mu = 0.8, se = 0.0)$ | 80% of these deaths assumed to take place in the care home (the remaining 20% in hospital). ¹⁴ |
| $m_{\delta rvn}$ | Relative death rate in residential vs nursing care homes | $\sim Beta(\mu = 0.47, se = 0.0)$ | See Supplementary material A3. |
| κ | Hospitalisation rate pppd for residents without COVID-19 clinical infection | Baseline (medium community prevalence scenario): $\sim Gamma(\mu = 0.00132, k = 10)$; low community prevalence scenario: $\sim Gamma(\mu = 0.00130, k = 10)$; high | See Supplementary material A1. |

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| | | community prevalence scenario: \sim $\text{Gamma}(\mu = 0.00104, k = 10)$ | |
| p_{survival} | Probability of residents with COVID-19 clinical infection returning to the care home from hospital having survived | $\sim \text{Beta}(\mu = 0.7, se = 0.1)$ | SUS data showed a mean of 30% of patients admitted to hospital for COVID died in hospital (see Supplementary material A4 for details). |
| $p_{EI \text{ non-COVID-19 } H}$ | Proportion of hospital discharges that enter the care home infected states (E, Ipc, Ia) (residents that didn't go to hospital symptomatic for COVID-19) | Baseline (medium community prevalence scenario): $\sim \text{Beta}(\mu = 0.01, se = 0.001)$; low community prevalence scenario: $\sim \text{Beta}(\mu = 0.007, se = 0.001)$; high community prevalence scenario: $\sim \text{Beta}(\mu = 0.004, se = 0.001)$ | Mean prevalence in each of the model compartments exiting hospital from the Evans et al. 2020 mathematical model on the 2020-05-01 (baseline, medium community prevalence scenario), 2020-07-15 (low community prevalence scenario) or 2020-04-01 (high community prevalence scenario). ¹⁵ |
| $p_{E, EI \text{ non-COVID-19 } H'}$ $p_{Ipc, EI \text{ non-COVID-19 } H'}$ $p_{Ia, EI \text{ non-COVID-19 } H}$ | Proportion of infected hospital discharges that enter the care home exposed (E), infectious preclinical (Ipc), and asymptomatic (Ia) states (residents that didn't go to hospital symptomatic for COVID-19) | Baseline (medium community prevalence scenario): 69% exposed, 13% infectious pre-clinical, 18% asymptomatic; low community prevalence scenario: 59% exposed, 14% infectious pre-clinical, 27% asymptomatic; high community prevalence scenario: 74% exposed, 11% infectious pre-clinical, 15% asymptomatic. | Mean prevalence in each of the model compartments exiting hospital from the Evans et al. 2020 mathematical model on the 2020-05-01 (baseline, medium community prevalence scenario), 2020-07-15 (low community prevalence scenario) or 2020-04-01 (high community prevalence scenario). ¹⁵ |
| $p_{R \text{ non-COVID-19 } H}$ | Proportion of hospital discharges that enter the care home recovered (R) state (residents that didn't go to hospital | Baseline (medium community prevalence scenario): $\sim \text{Beta}(\mu = 0.05, se = 0.0)$; low community prevalence scenario: \sim | Assuming the mean ratio of susceptible to recovered was the same as in the community (informed by median of 500 runs in England from |

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| | symptomatic for COVID-19) | $Beta(\mu = 0.06, se = 0.0)$; high community prevalence scenario: $\sim Beta(\mu = 0.02, se = 0.0)$ | Davies et al. 2020 model fit to data from the community ⁵). This ratio was applied to $(1 - p_{I non-COVID-19 H})$, estimated as above. |
| $p_{S non-COVID-19 H}$ | Proportion of hospital discharges that enter the care home susceptible (S) state (residents that didn't go to hospital symptomatic for COVID-19) | $1 - (p_{R non-COVID-19 H} + p_{EI non-COVID-19 H})$ | |
| $p_{Icl COVID-19 H}$ | Proportion of hospital discharged residents that enter the care home still residually shedding ie. in state of clinical infection with low infectiousness (Icl) vs recovered (R) state (residents that went to hospital symptomatic for COVID-19) | $\sim Beta(\mu = 0.06, se = 0.0)$ | Assuming on average 6% were still shedding at 14 days ⁴ , when they were assumed to (on average) be discharged. In the baseline scenario, those testing positive upon hospital discharge test were immediately isolated upon their return to the care home (Icli compartment). |
| $p_{EI s2}$ | Proportion of replacement staff who enter the care home infected states (E, Ipc, Ia) | Baseline (medium community prevalence scenario): $\sim Beta(\mu = 0.005, se = 0.001)$; low community prevalence scenario: $\sim Beta(\mu = 0.0008, se = 0.001)$; high community prevalence scenario: $\sim Beta(\mu = 0.02, se = 0.001)$ | Assumed the same as in the community. Informed by median of 500 runs in England from Davies et al. 2020 model ⁵ on the 2020-09-30 (baseline, medium community prevalence scenario), 2020-07-15 (low community prevalence scenario) or 2020-04-01 (high community prevalence scenario). |
| $p_{E, EI s2'}$ $p_{Ipc, EI s2'}$ $p_{Ia, EI s2}$ | Proportion of infected replacement staff who enter the care home exposed (E), infectious | Baseline (medium community prevalence scenario): 44% exposed, 12% infectious pre-clinical, 44% asymptomatic; | Assumed the same as in the community. Informed by median of 500 runs in England from Davies et al. 2020 model ⁵ on the |

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| | preclinical (Ipc), and asymptomatic (Ia) states | low community prevalence scenario: 39% exposed, 15% infectious pre-clinical, 46% asymptomatic; high community prevalence scenario: 38% exposed, 10% infectious pre-clinical, 52% asymptomatic. | 2020-09-30 (baseline, medium community prevalence scenario), 2020-07-15 (low community prevalence scenario) or 2020-04-01 (high community prevalence scenario). |
| p_{Rs2} | Proportion of replacement staff who enter the care home recovered (R) state | Baseline (medium community prevalence scenario): $\sim Beta(\mu = 0.13, se = 0.01)$; low community prevalence scenario: $\sim Beta(\mu = 0.11, se = 0.01)$; high community prevalence scenario: $\sim Beta(\mu = 0.04, se = 0.01)$ | Assumed the same as in the community. Informed by median of 500 runs in England from Davies et al. 2020 model ⁵ on the 2020-09-30 (baseline, medium community prevalence scenario), 2020-07-15 (low community prevalence scenario) or 2020-04-01 (high community prevalence scenario). |
| p_{Ss2} | Proportion of replacement staff who enter the care home susceptible (S) state | $1 - (p_{Rs2} + p_{EIs2})$ | |
| Parameters relating to testing and isolation | | | |
| $1/\gamma_c$ or $delay_isolation_c$ | Delay to isolation/absence in symptomatic residents/staff (days) | Baseline: $Gamma(\mu = 1, k = 4)$ | Assumed (baseline scenario). |
| $1/\gamma_{nc}$ or $delay_isolation_nc$ | Delay to isolation/absence in residents/staff with preclinical infection or asymptomatic infection testing positive (days) | Baseline: $Gamma(\mu = 2, k = 4)$ | Assumed (baseline scenario). |
| p_{tnc} | Probability of residents without COVID-19 clinical infection being tested | Baseline: $\sim Beta(\mu = 0.85, se = 0.01)$ | Assumed (baseline scenario). |

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| p_{tncs} | Probability of staff without COVID-19 clinical infection being tested | Baseline: $\sim Beta(\mu = 0.95, se = 0.05)$ | Assumed (baseline scenario). |
| p_{tc} | Probability of residents with COVID-19 clinical infection being tested | Baseline: $\sim Beta(\mu = 0.9, se = 0.05)$ | Assumed (baseline scenario). |
| f_{tnc} | Frequency of testing residents without COVID-19 clinical infection (days) | Baseline: 28 | Assumed (baseline scenario). |
| f_{tncs} | Frequency of testing staff without COVID-19 clinical infection (days) | Baseline: 7 | Assumed (baseline scenario). |
| f_{tc} | Frequency of testing residents with COVID-19 clinical infection (days) | Baseline: 0 (testing on the day of symptom onset) | Assumed (baseline scenario). |
| p_{fn} | Probability of false negative PCR result in care home | $\sim Beta(\mu = 0.2, se = 0.05)$ | About 90% PCR tests are positive in individuals with early stage COVID-19 clinical infection. ^{16,17} However, assuming this is lower as staff are testing. |
| p_{fnh} | Probability of false negative PCR result in hospital | $\sim Beta(\mu = 0.1, se = 0.01)$ | About 90% PCR tests are positive in individuals with early stage COVID-19 clinical infection. ^{16,17} |
| p_i | Probability of residents with COVID-19 clinical infection or a positive test being isolated | $\sim Beta(\mu = 0.8, se = 0.08)$ | Assumed. |
| $p_{replaced}$ | Probability of absent staff being replaced | $\sim Beta(\mu = 0.8, se = 0.05)$ | Assumed. |

Unless otherwise indicated, values assumed the same for nursing and residential care homes.

SUPPLEMENTARY FIGURES

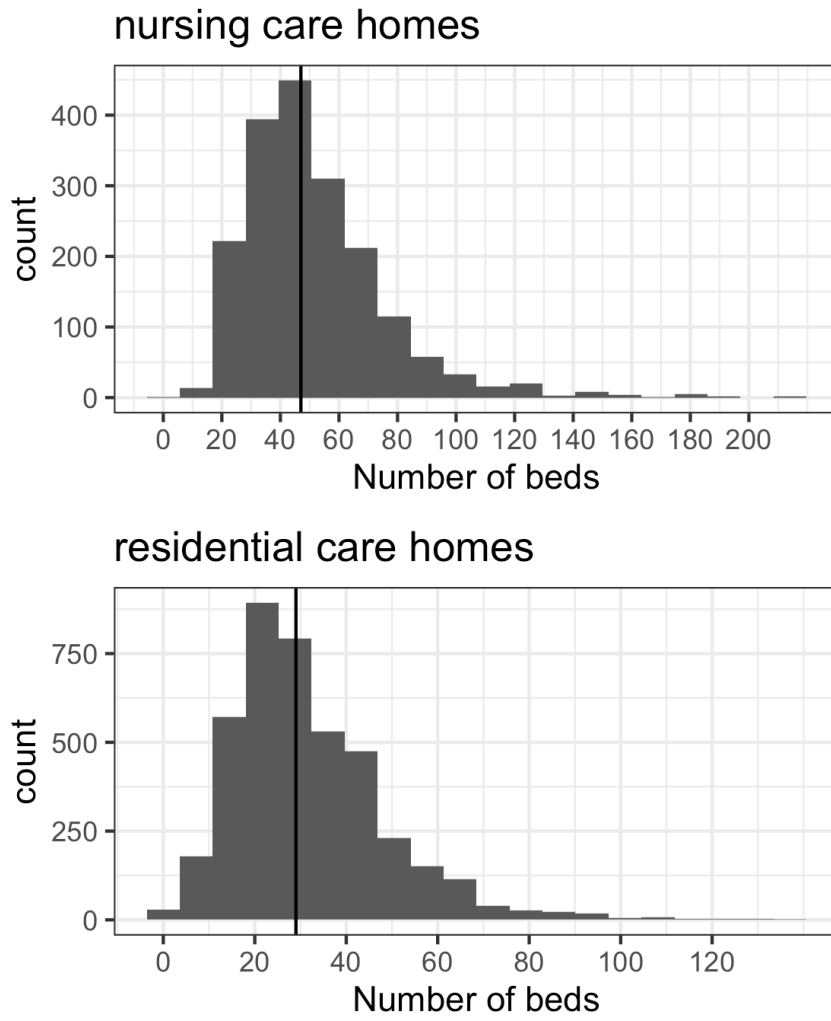


Figure S1. Number of beds in nursing (top) and residential (bottom) care homes housing only older residents in England. Source: CQC database.

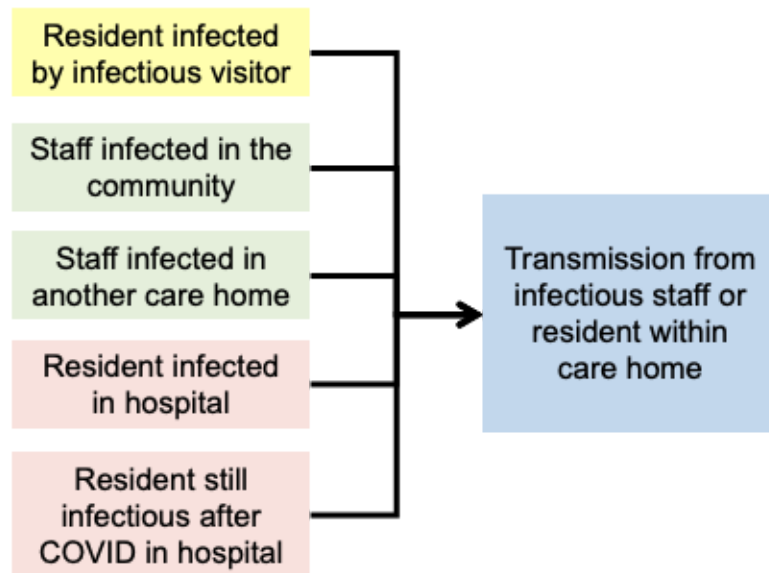


Figure S2. Pathways by which care home residents and staff may become infected.

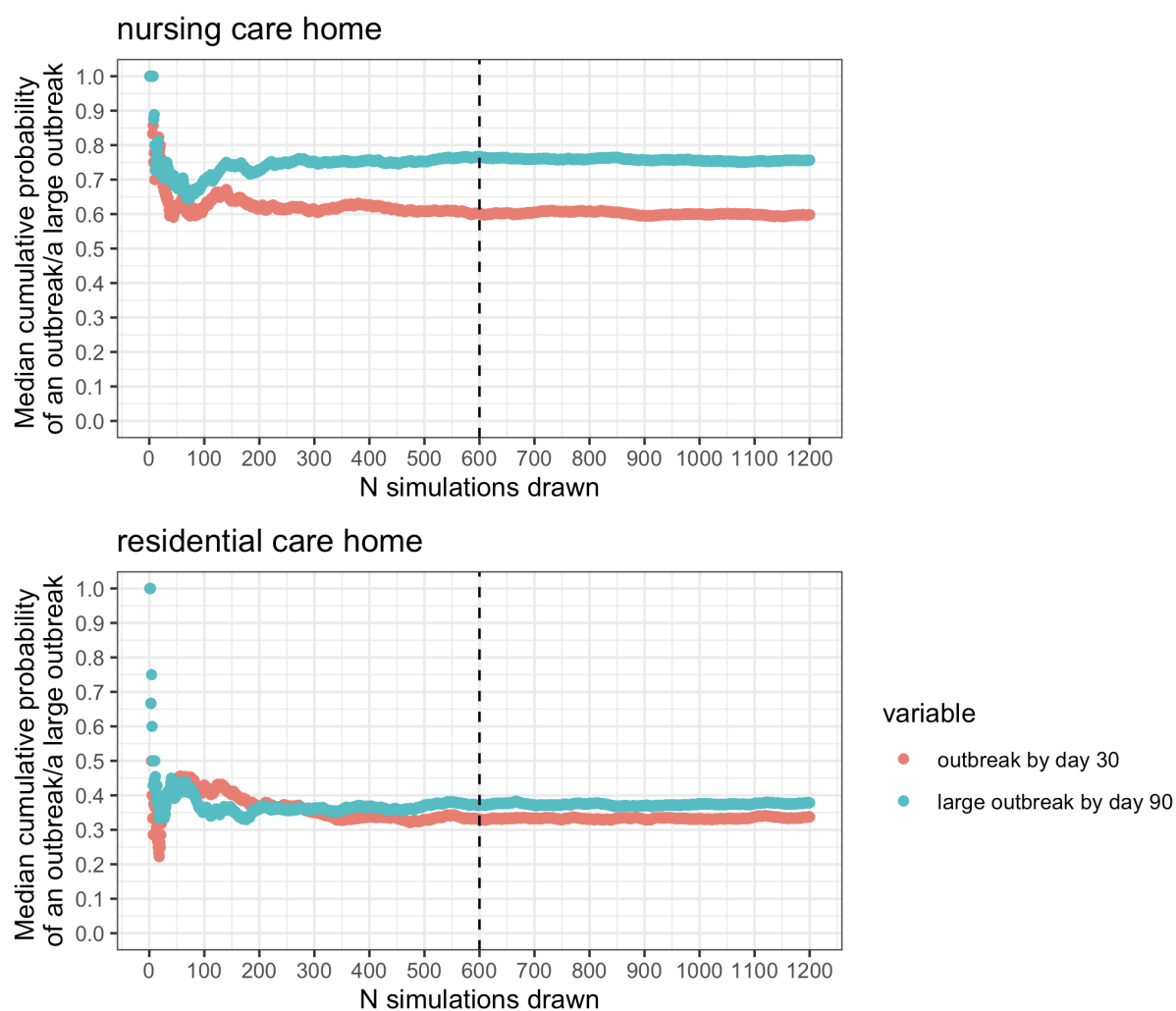


Figure S3. Cumulative probability of an outbreak by day 30 (red) and a large outbreak by day 90 (blue) in a nursing care home (top plot) and a residential care home (bottom plot) by the number of simulations run for a single parameter set. The dashed line represents the number of simulations carried out for each parameter set.

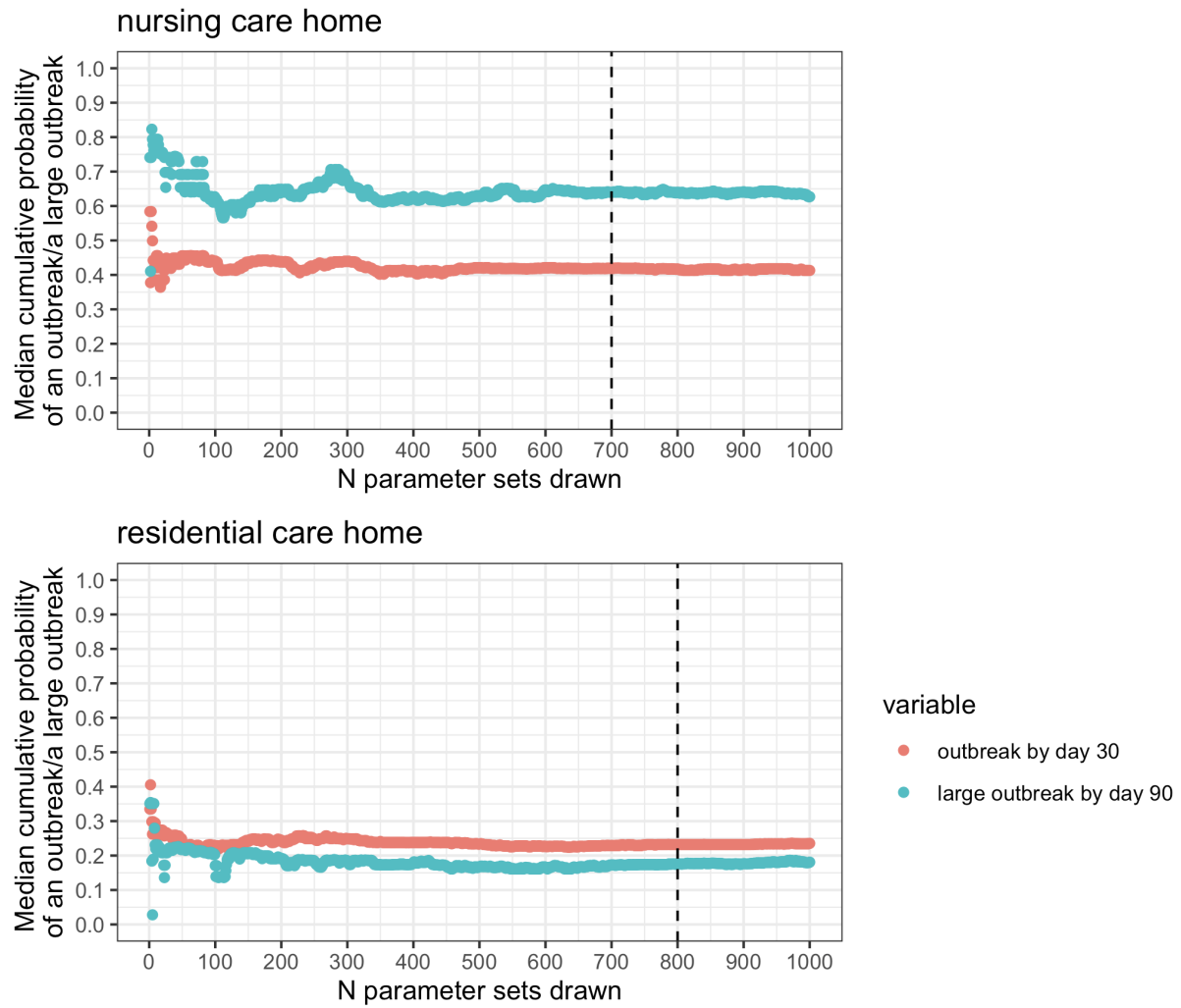


Figure S4. Cumulative probability of an outbreak by day 30 (red) and a large outbreak by day 90 (blue) in a nursing care home (top plot) and a residential care home (bottom plot) by the number of parameter sets drawn. The dashed line represents the number of parameter sets simulated.

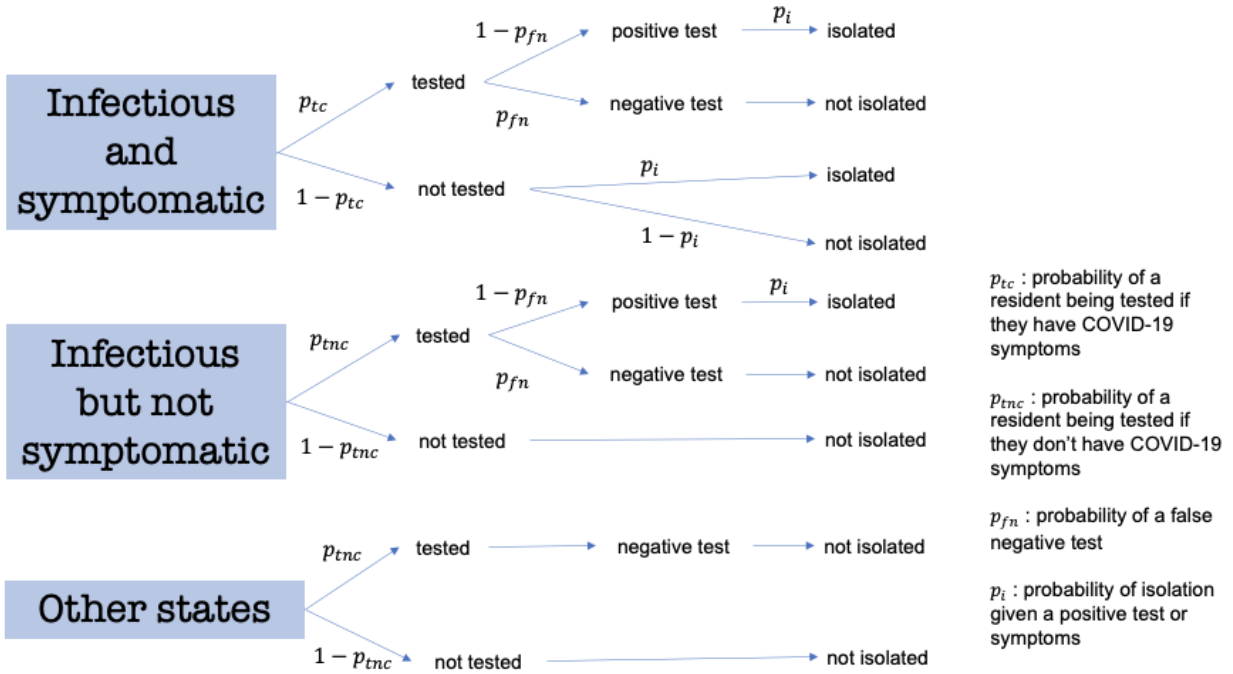


Figure S5. Testing and isolation pathway for care home residents. Isolation was assumed to be implemented within the care home. The effectiveness of isolation was, on average, 75%.

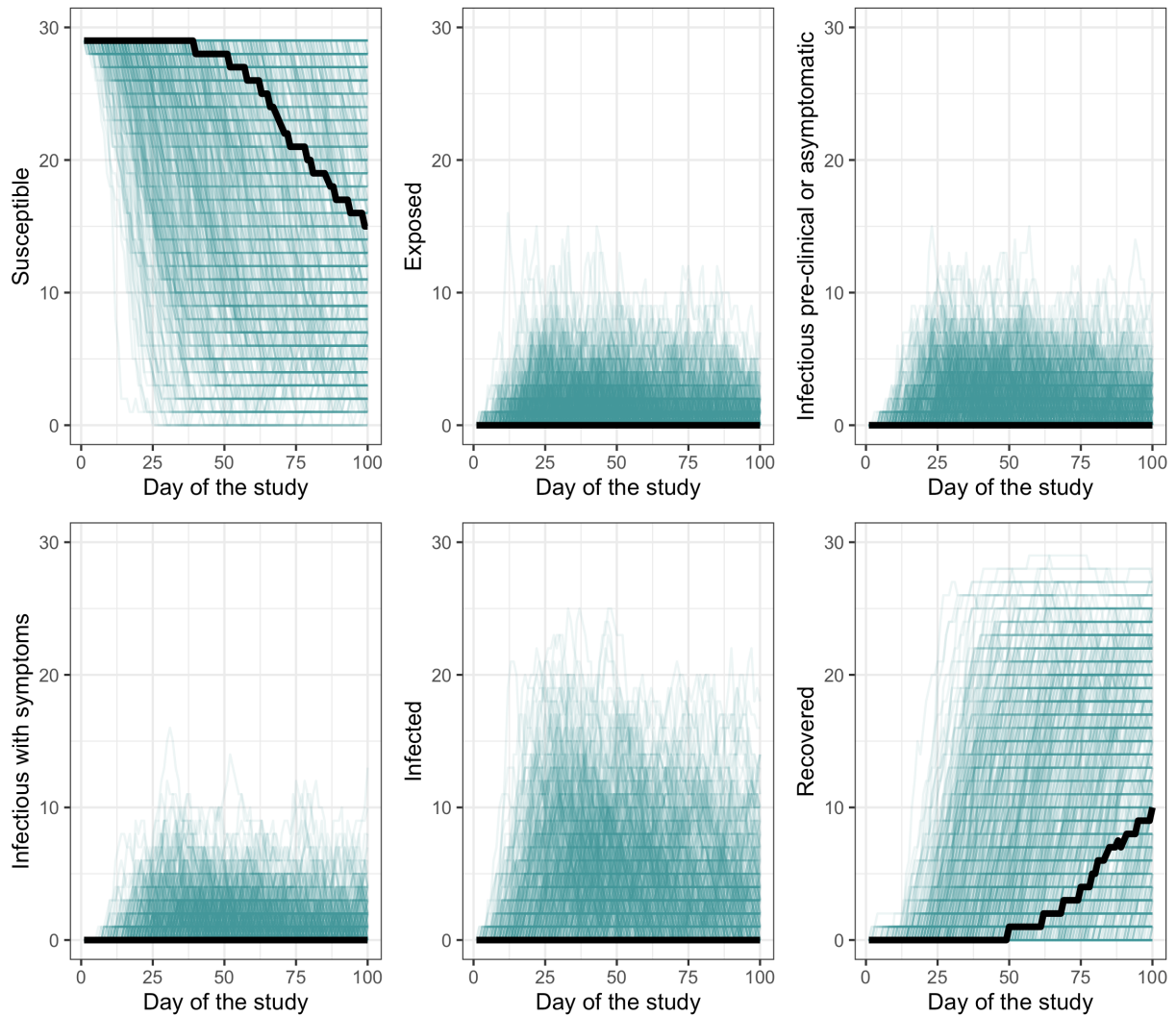


Figure S6. Care home residents: 1000 model runs by infection state of residents in a residential care home. Infected residents were those either exposed, infectious preclinical, asymptomatic, or symptomatic. The black line represents the median values over time. Day 0 of the study was the day at which the simulations were initialised. Each colour indicates a different run of the model.

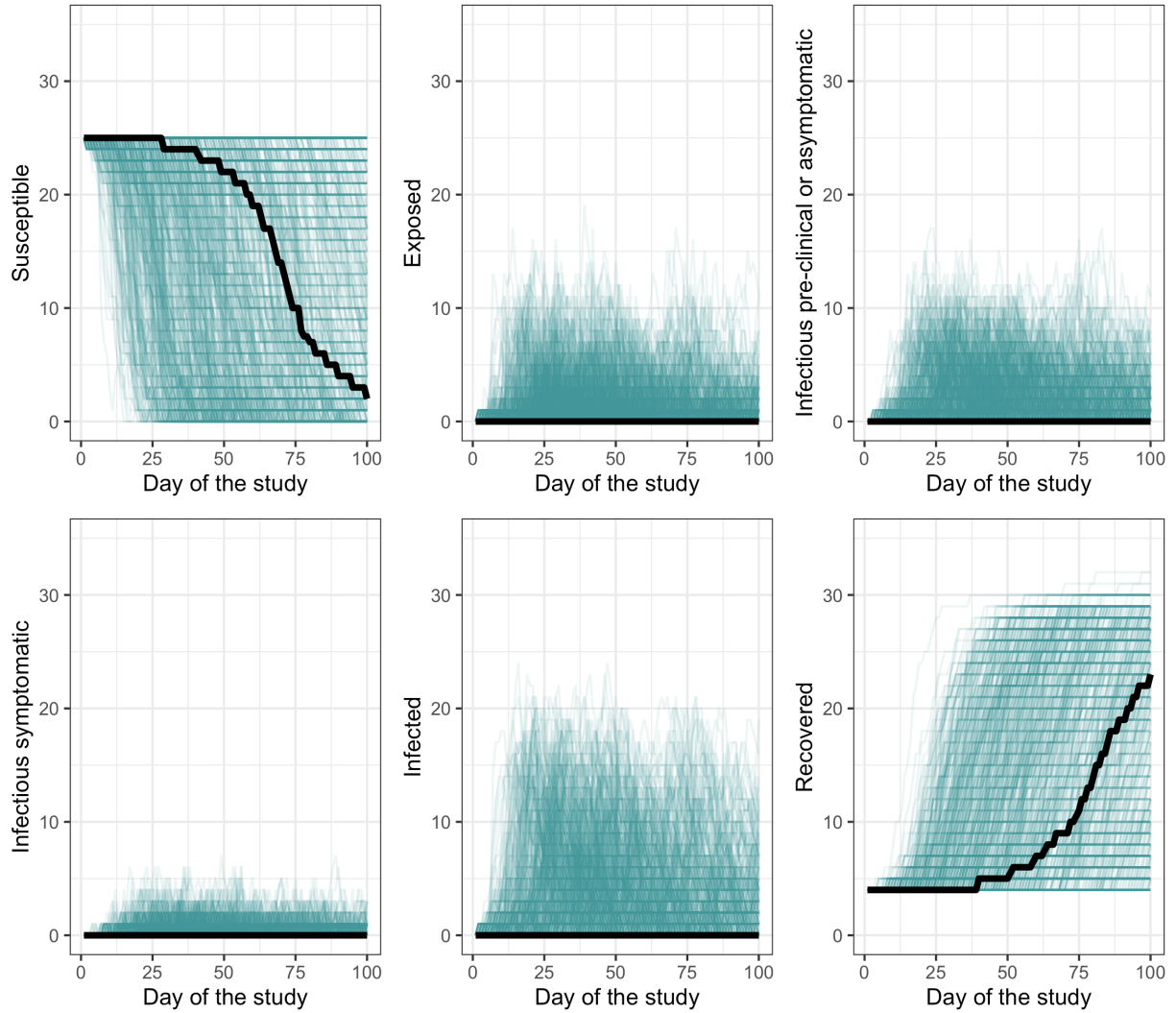


Figure S7. Care home staff: 1000 model runs by infection state of staff in a residential care home. Infected staff were those either exposed, infectious preclinical, asymptomatic, or symptomatic. The black line represents the median values over time. Day 0 of the study was the day at which the simulations were initialised. Each colour indicates a different run of the model.

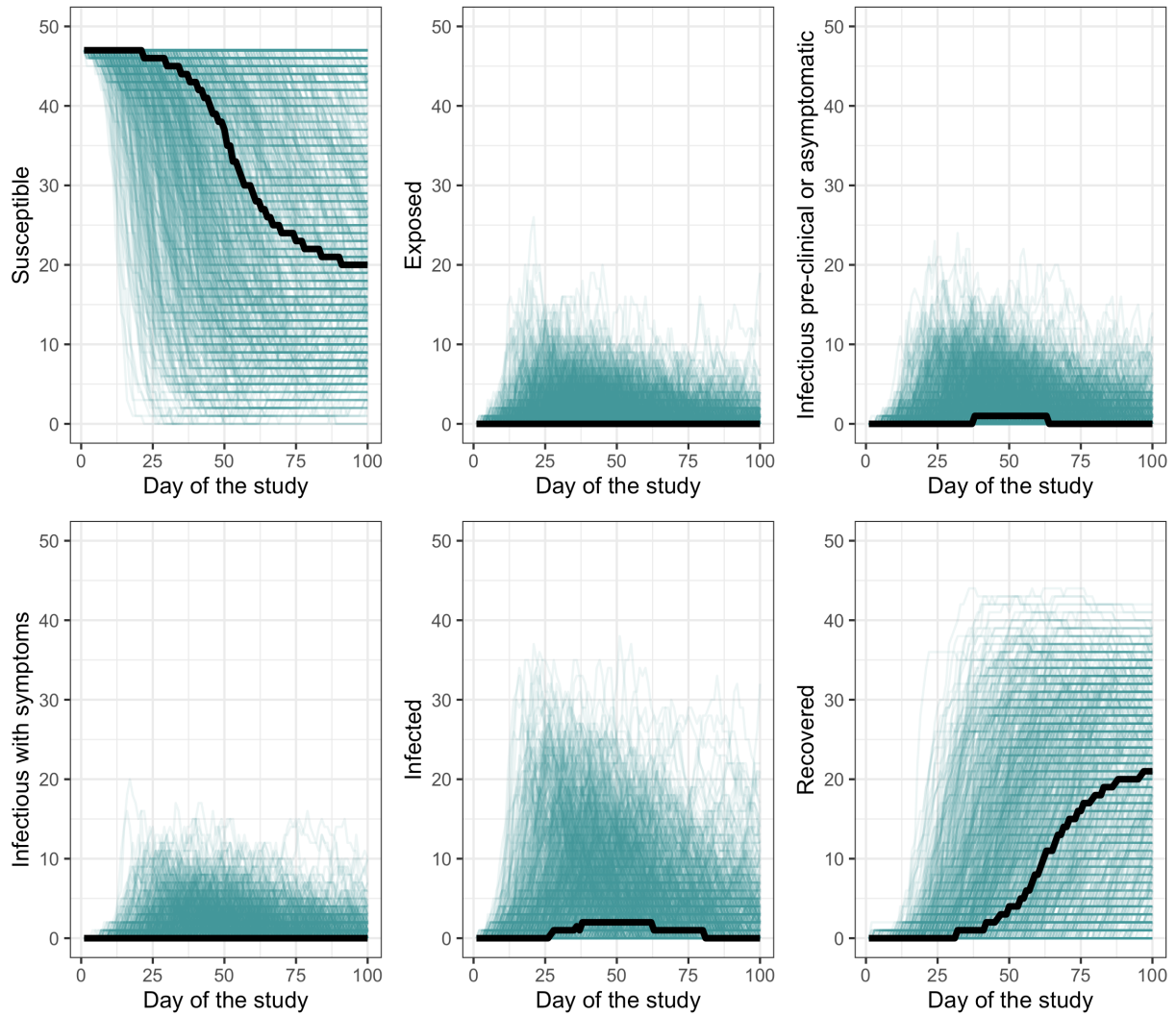


Figure S8. Care home residents: 1000 model runs by infection state of residents in a nursing care home. Infected residents were those either exposed, infectious preclinical, asymptomatic, or symptomatic. The black line represents the median values over time. Day 0 of the study was the day at which the simulations were initialised. Each colour indicates a different run of the model.

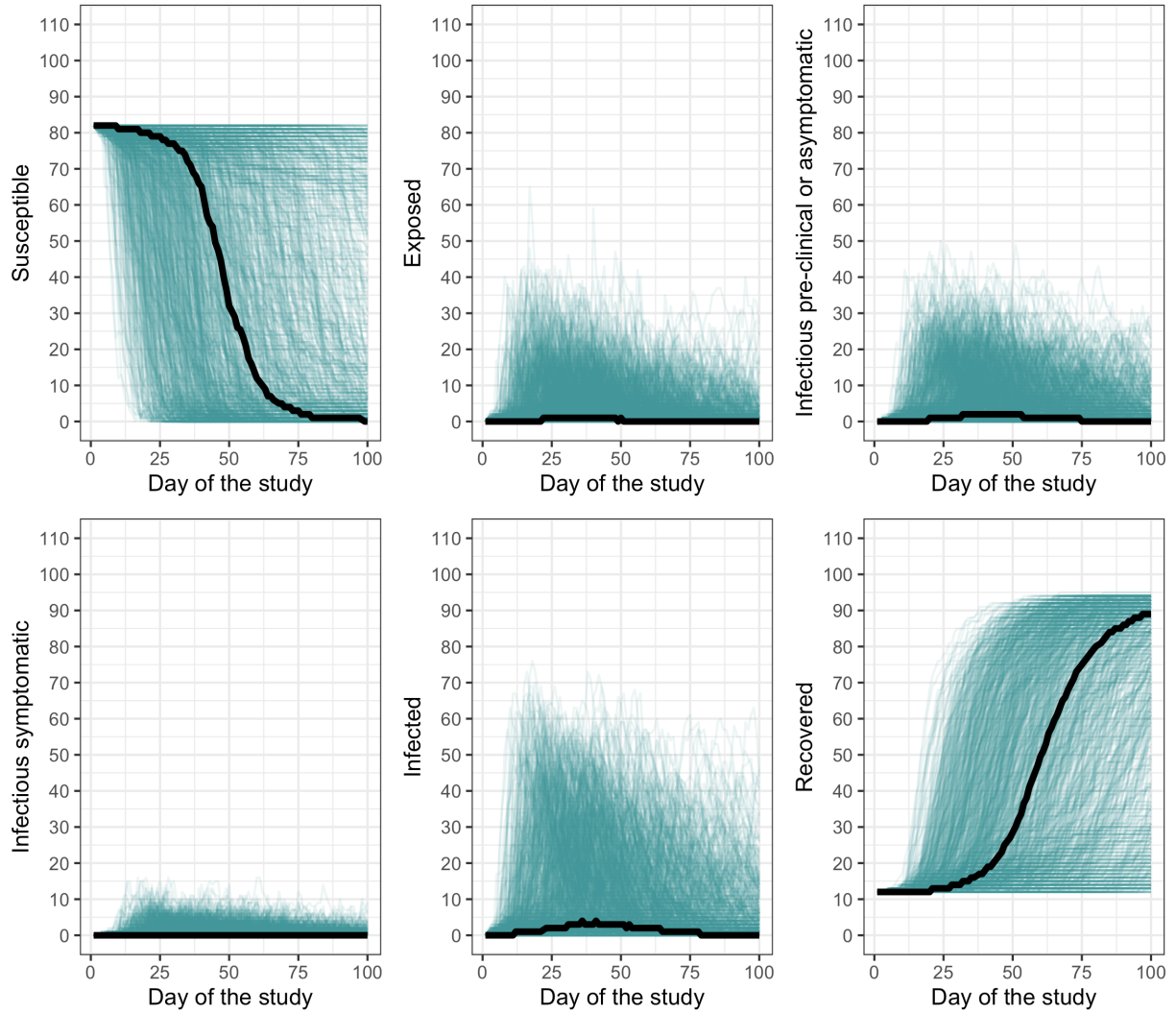


Figure S9. Care home staff: 1000 model runs by infection state of staff in a nursing care home. Infected staff were those either exposed, infectious preclinical, asymptomatic, or symptomatic. The black line represents the median values over time. Day 0 of the study was the day at which the simulations were initialised. Each colour indicates a different run of the model.

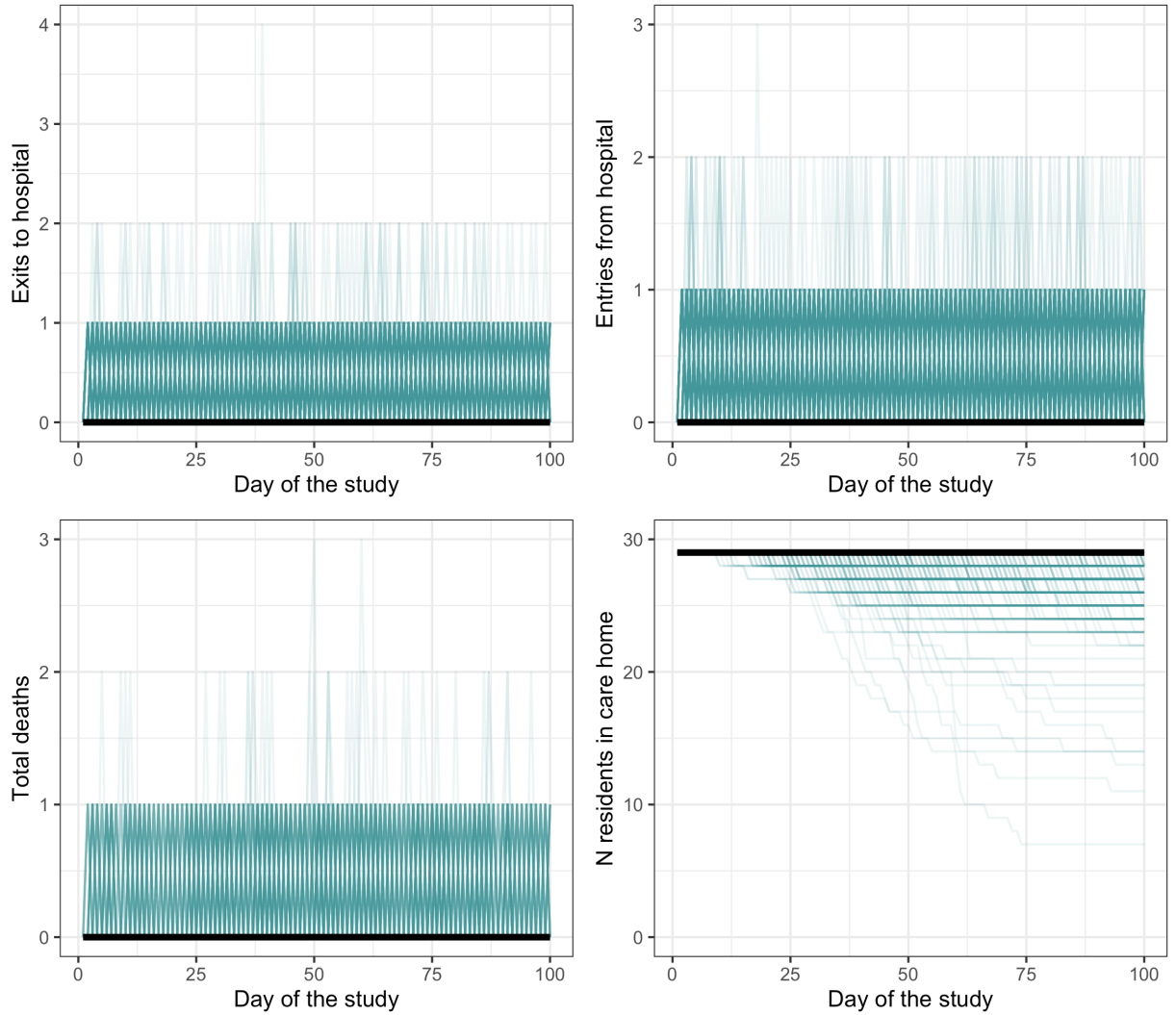


Figure S10. Resident population in a residential care home for 1000 model runs. The left top panel shows the number of daily exits from the care home to hospital; the right top panel shows the number of daily entries from hospital to the care home, the bottom left panel shows the number of daily deaths in the care home, and the bottom right panel shows the number of residents in the care home each day of the study. The black line represents the median values over time. Day 0 of the study was the day at which the model simulations were initialised. Each colour indicates a different run of the model.

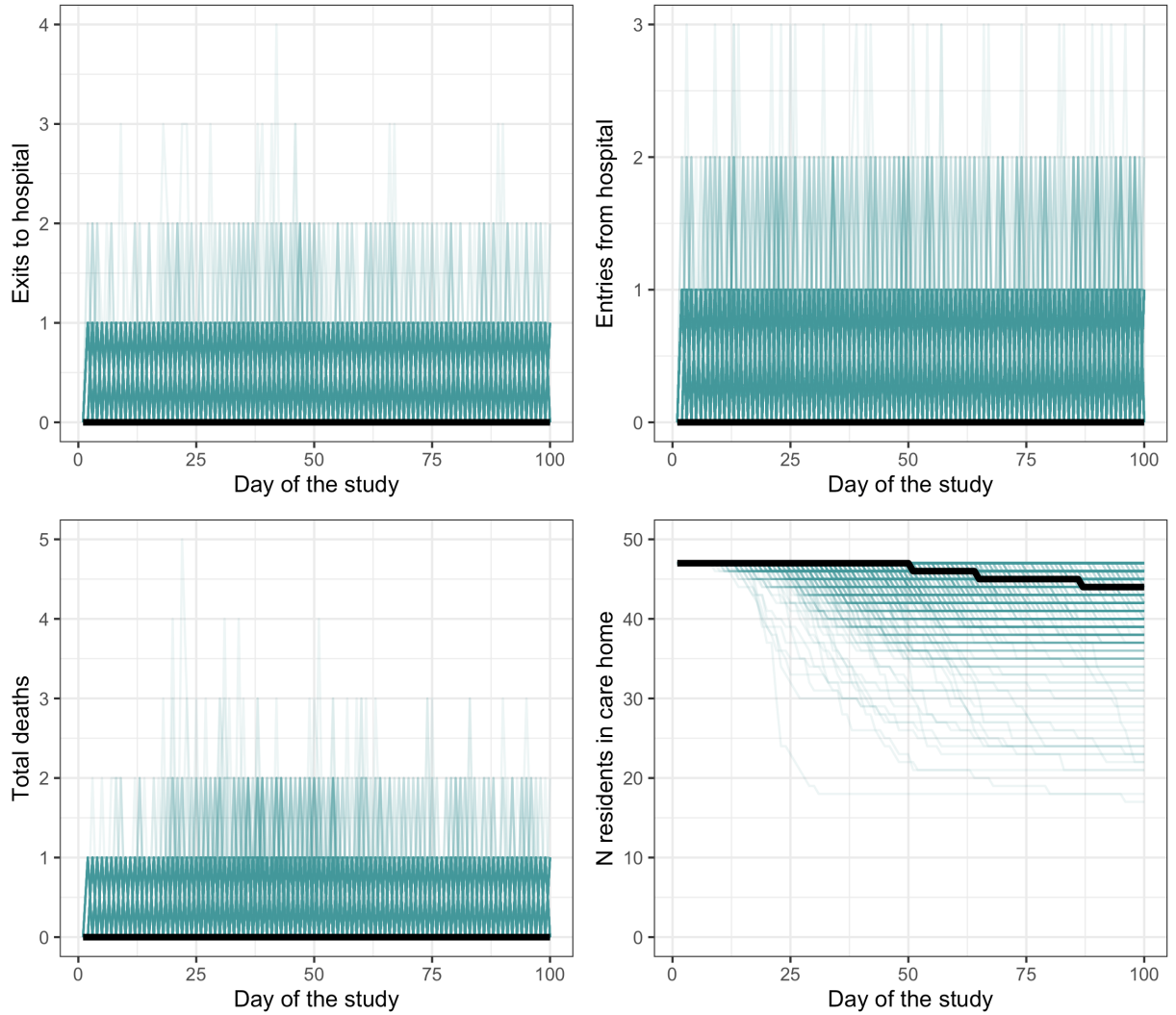


Figure S11. Resident population in a nursing care home for 1000 model runs. The left top panel shows the number of daily exits from the care home to hospital; the right top panel shows the number of daily entries from hospital to the care home, the bottom left panel shows the number of daily deaths in the care home, and the bottom right panel shows the number of residents in the care home each day of the study. The black line represents the median values over time. Day 0 of the study was the day at which the model simulations were initialised. Each colour indicates a different run of the model.

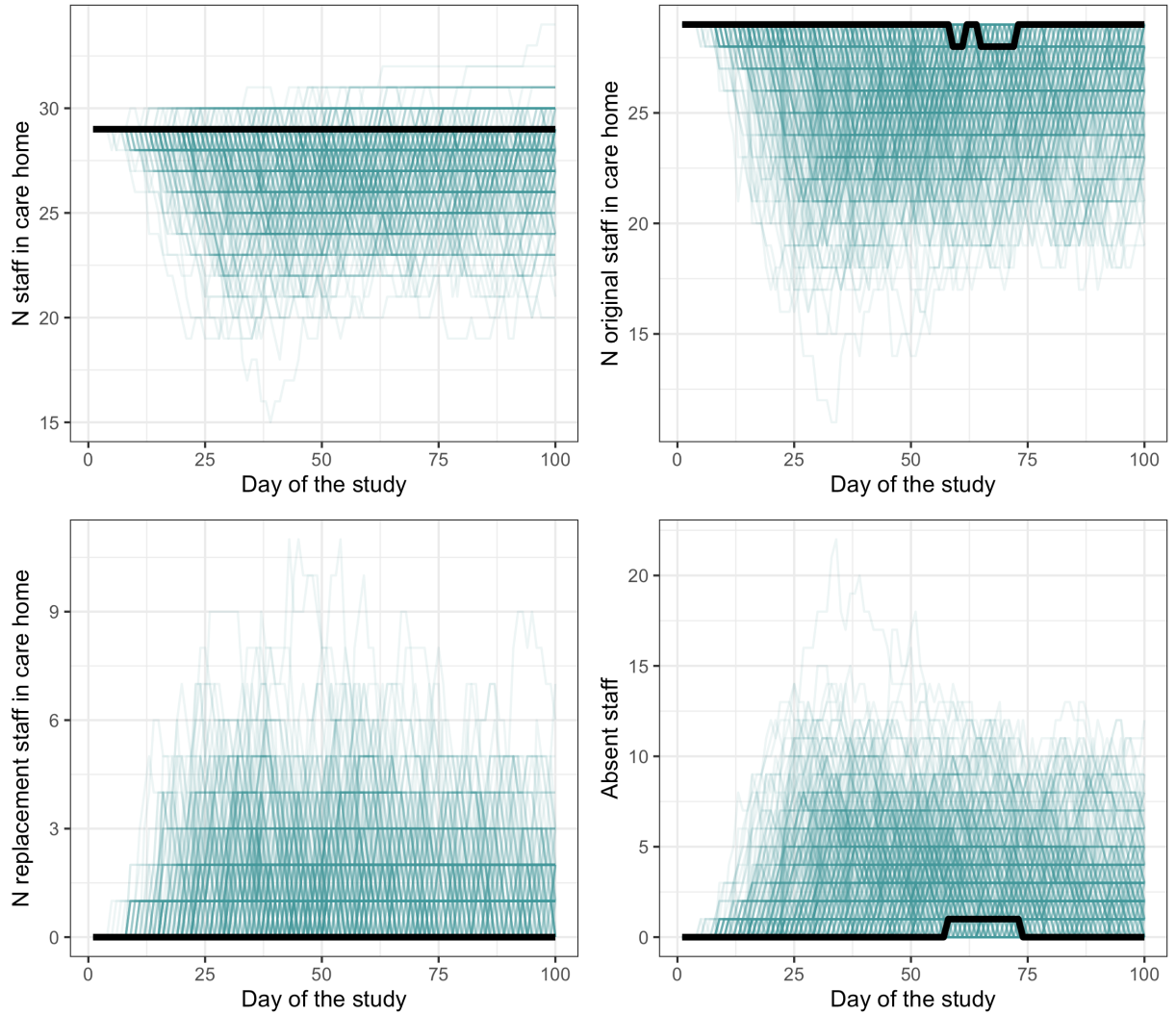


Figure S12. Staff population numbers in a residential care home for 1000 model runs. The left top panel shows the number of staff in the care home on each day of the study; the right top panel shows the number of original staff in the care home on each day of the study, the bottom left panel shows the number of replacement staff in the care home on each day of the study, and the bottom right panel shows the number of staff absent from the care home on each day of the study. The black line represents the median values over time. Day 0 of the study was the day at which the model simulations were initialised. Each colour indicates a different run of the model.

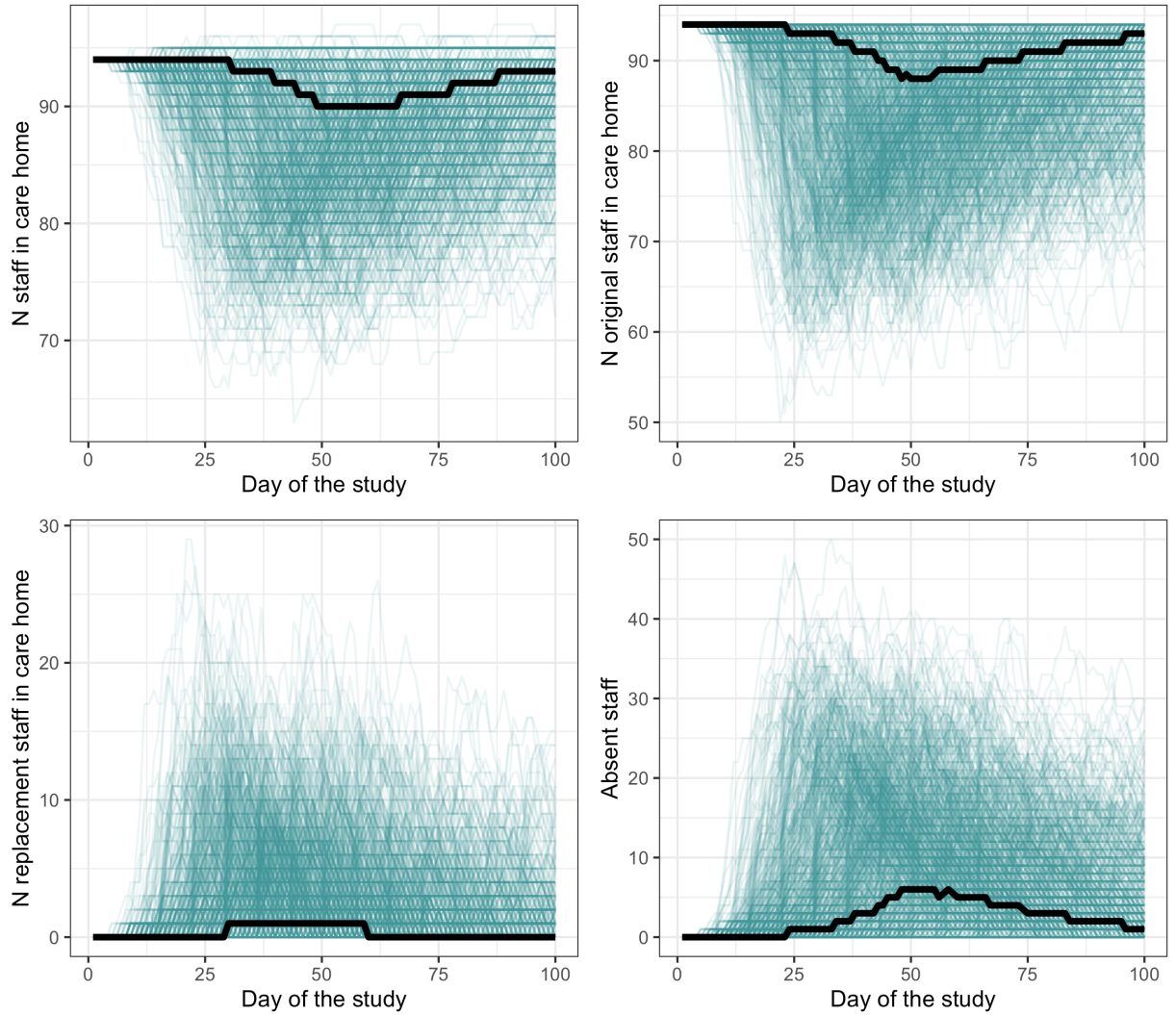


Figure S13. Staff population numbers in a nursing care home for 1000 model runs. The left top panel shows the number of staff in the care home on each day of the study; the right top panel shows the number of original staff in the care home on each day of the study, the bottom left panel shows the number of replacement staff in the care home on each day of the study, and the bottom right panel shows the number of staff absent from the care home on each day of the study. The black line represents the median values over time. Day 0 of the study was the day at which the model simulations were initialised. Each colour indicates a different run of the model.

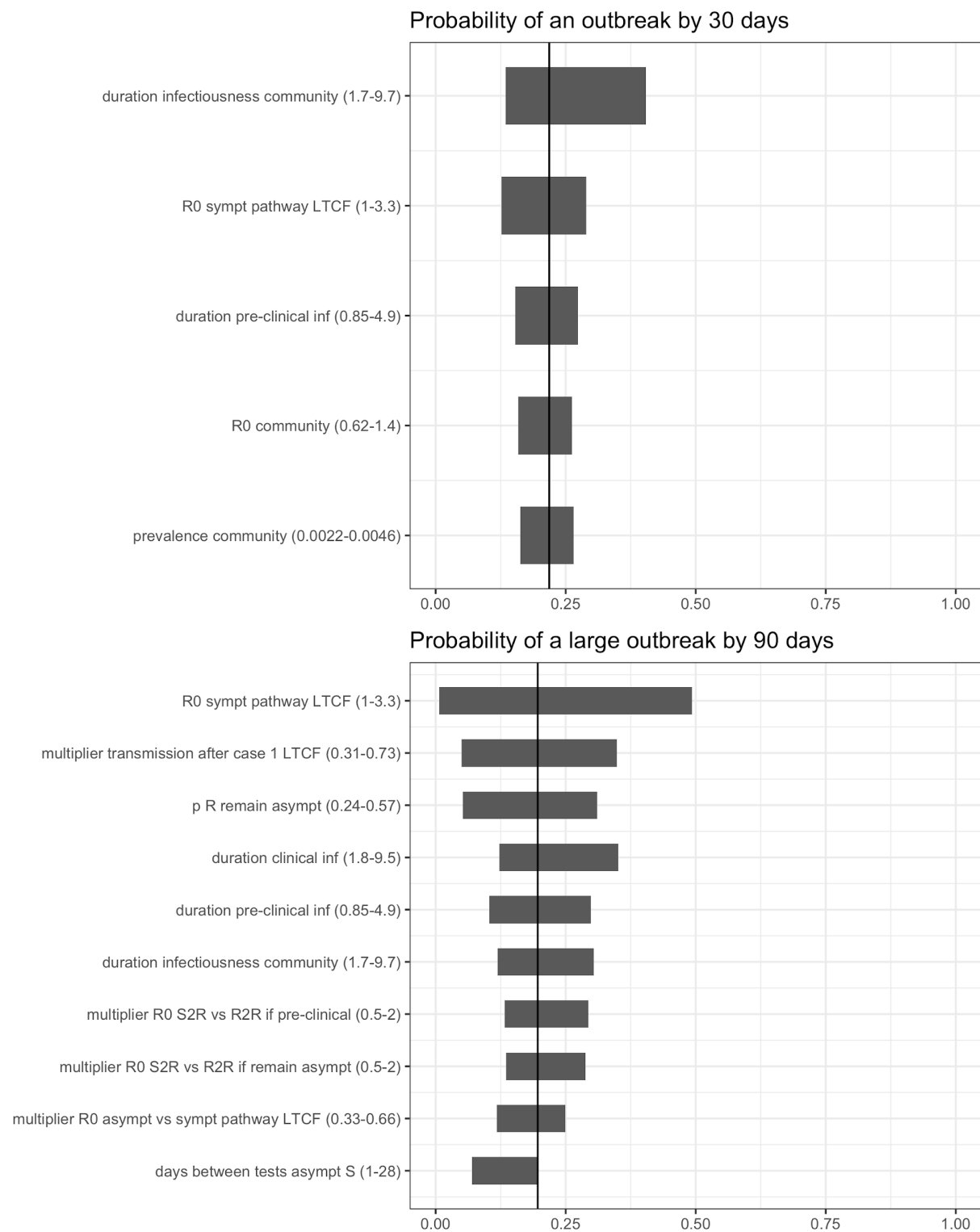


Figure S14. Sensitivity of model outcomes to model parameters in a residential care home. Only the parameters with the highest impact on model outcomes are shown (>0.1 difference). S=staff; R=resident.

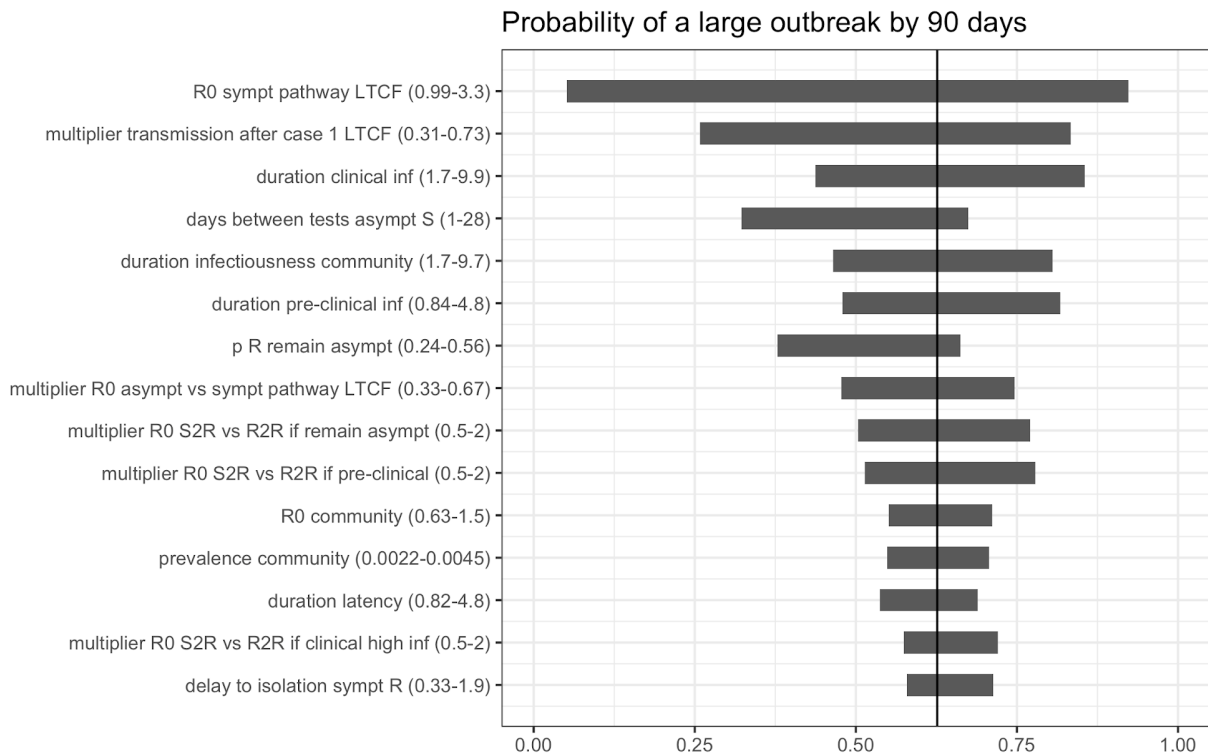
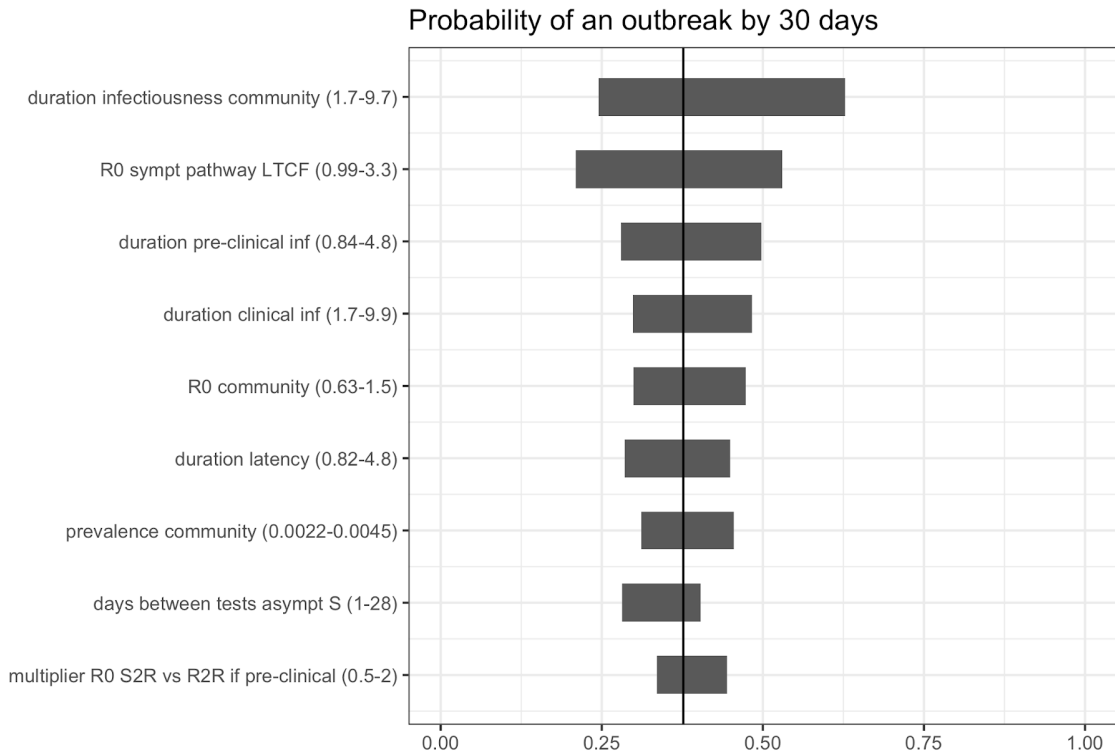


Figure S15. Sensitivity of model outcomes to model parameters in a nursing care home. Only the parameters with the highest impact on model outcomes are shown (>0.1 difference). S=staff; R=resident.

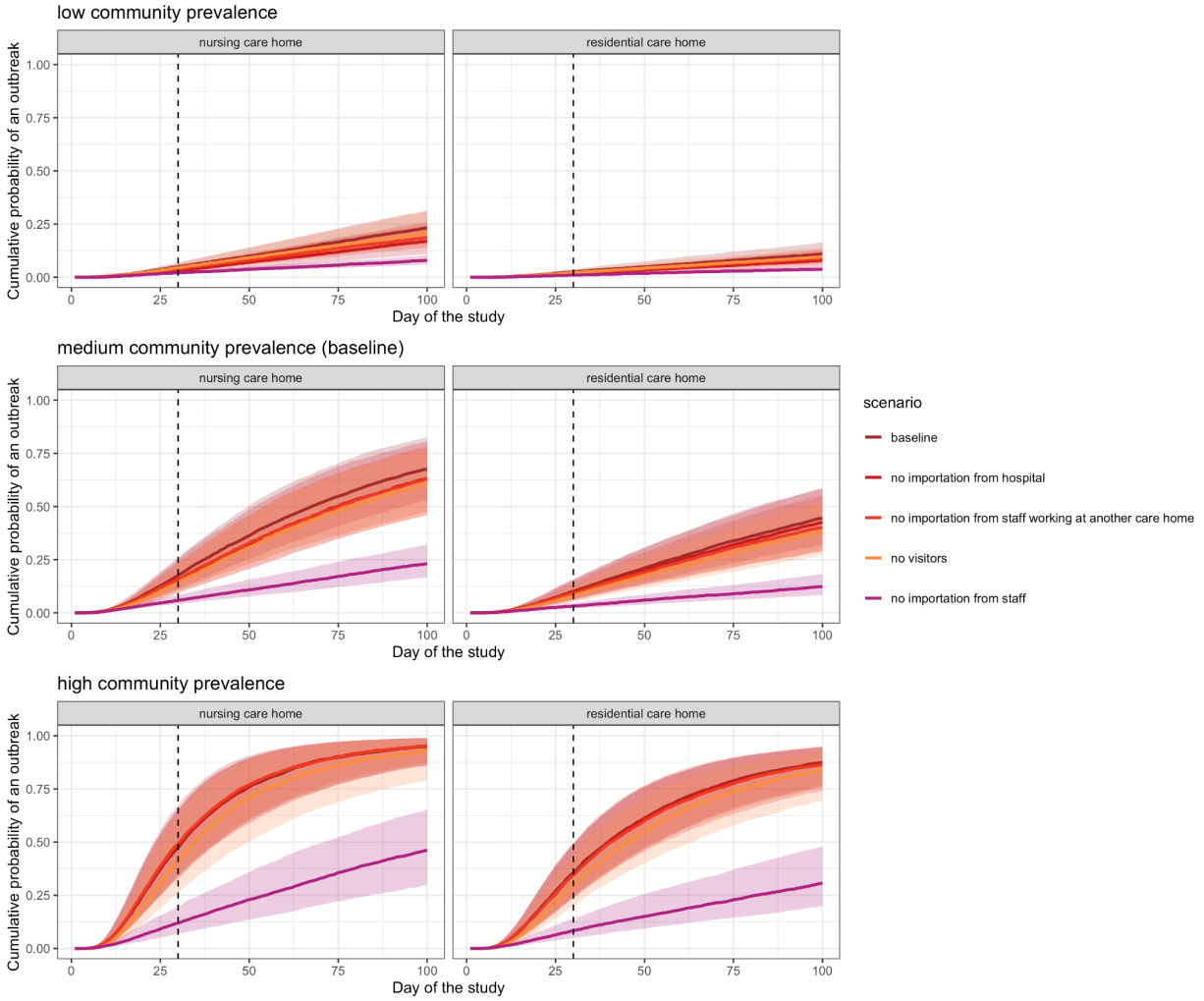


Figure S16. The cumulative probability of an outbreak at 30 days in a scenario where 50% of staff and residents are immune at the start of the simulation, under low community prevalence (top panels), medium community prevalence (middle panels) and high community prevalence (bottom panels) over time for different importation scenarios (dark brown=baseline, dark red=no importation from hospital, light red=no importation from staff working at another care home, orange=no visitors, purple=no importation from staff), in both nursing care homes (left panels) and residential care homes (right panels).

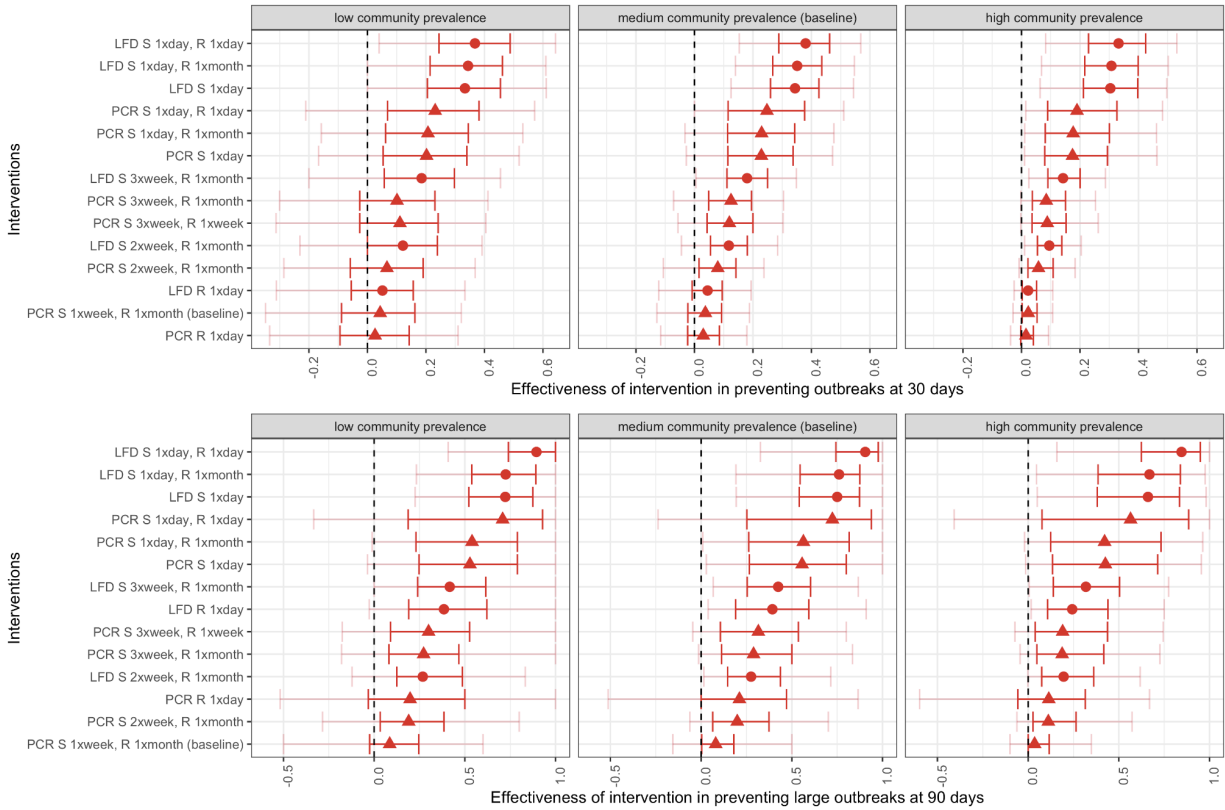


Figure S17. Effectiveness of testing strategies in preventing outbreaks in residential care homes at 30 days (top panels) and large outbreaks at 90 days (bottom panels) by testing intervention and under low (left panels), medium (baseline, middle panels) and high (right panels) community prevalence. In red, the 25-75%, in pink, the 5-95%. Testing interventions include PCR testing (triangles) and LFD testing (dots). R stands for resident and S for staff.

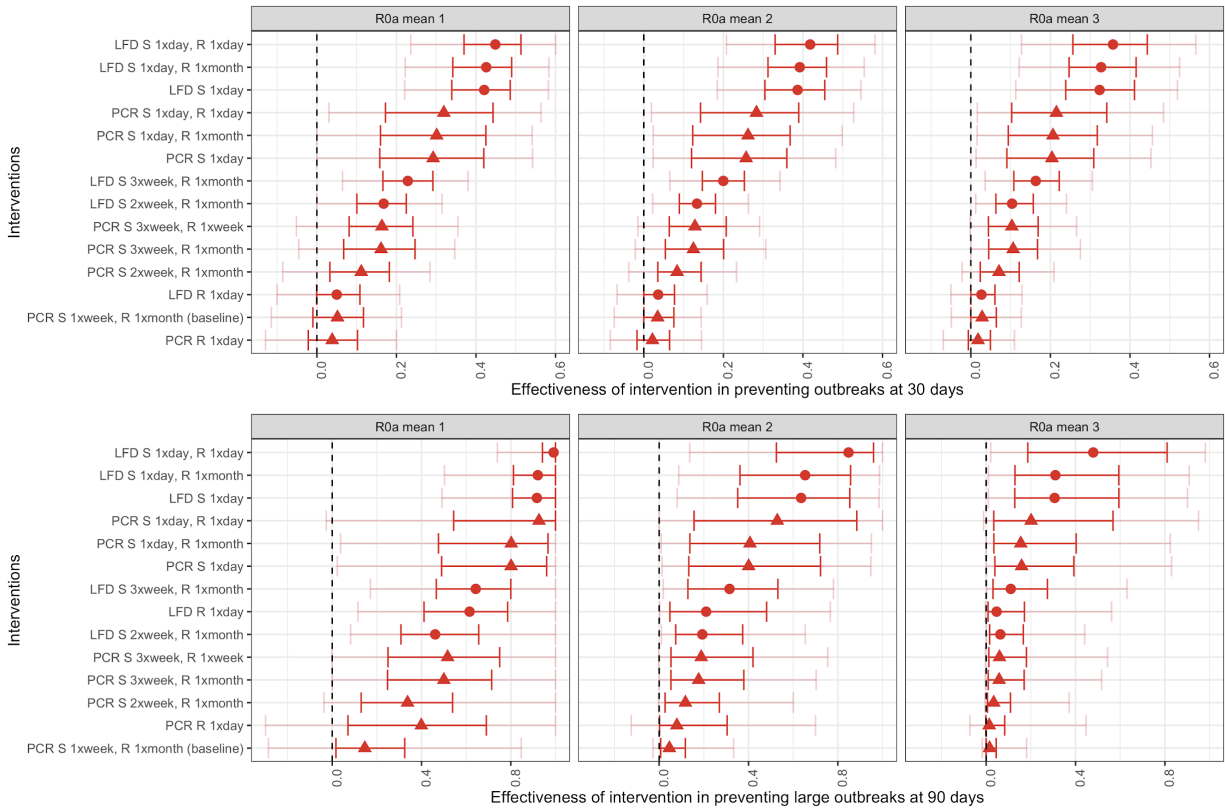


Figure S18. Effectiveness of testing strategies in preventing outbreaks in nursing care homes at 30 days (top panels) and large outbreaks at 90 days (bottom panels) by testing intervention and under $R_0a=1$ (left panels), $R_0a=2$ (baseline, middle panels) and $R_0a=3$ (right panels). R_0a was the average R_0 for individuals who were eventually symptomatic (pathway (a)). In red, the 25-75%, in pink, the 5-95%. Testing interventions include PCR testing (triangles) and LFD testing (dots). R stands for resident and S for staff.

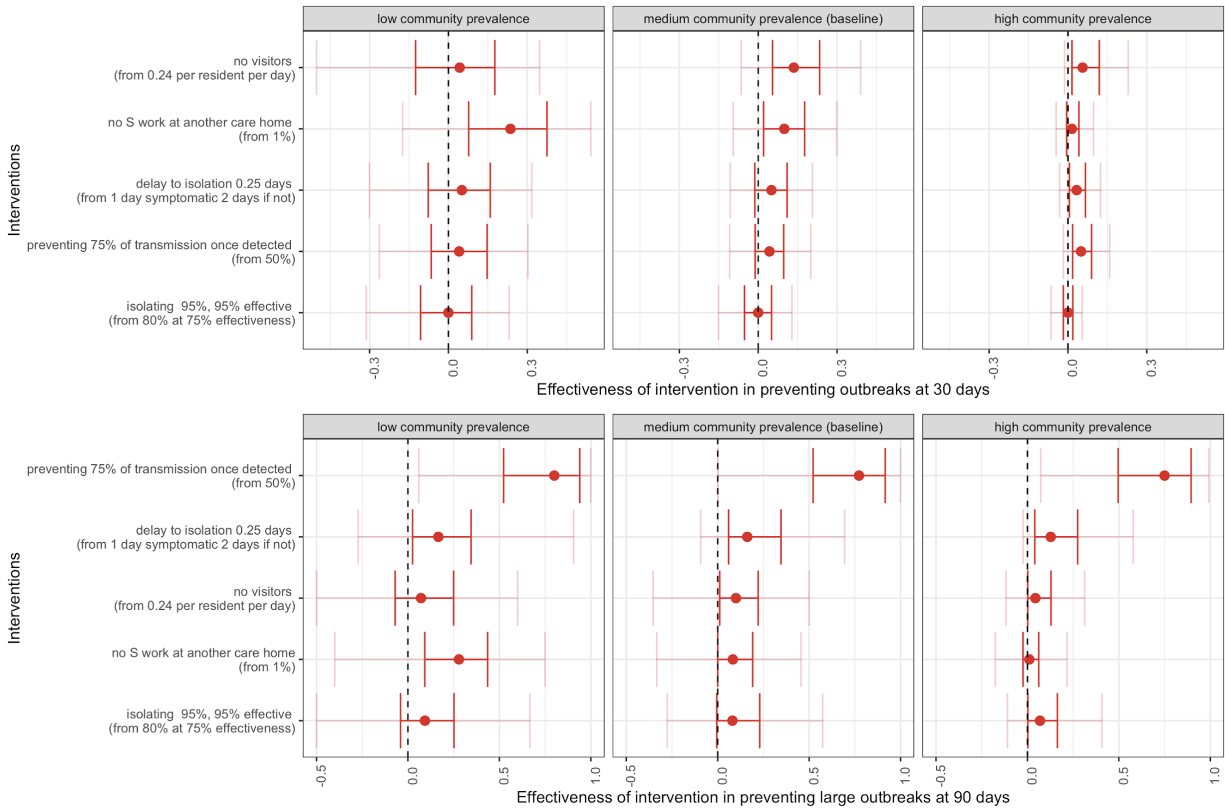


Figure S19. Effectiveness of interventions in preventing outbreaks in residential care homes at 30 days (top panels) and large outbreaks at 90 days (bottom panels) by low (left panels), medium (baseline, middle panels) and high (right panels) community prevalence. In red, the 25-75%, in pink, the 5-95%. R stands for resident and S for staff.

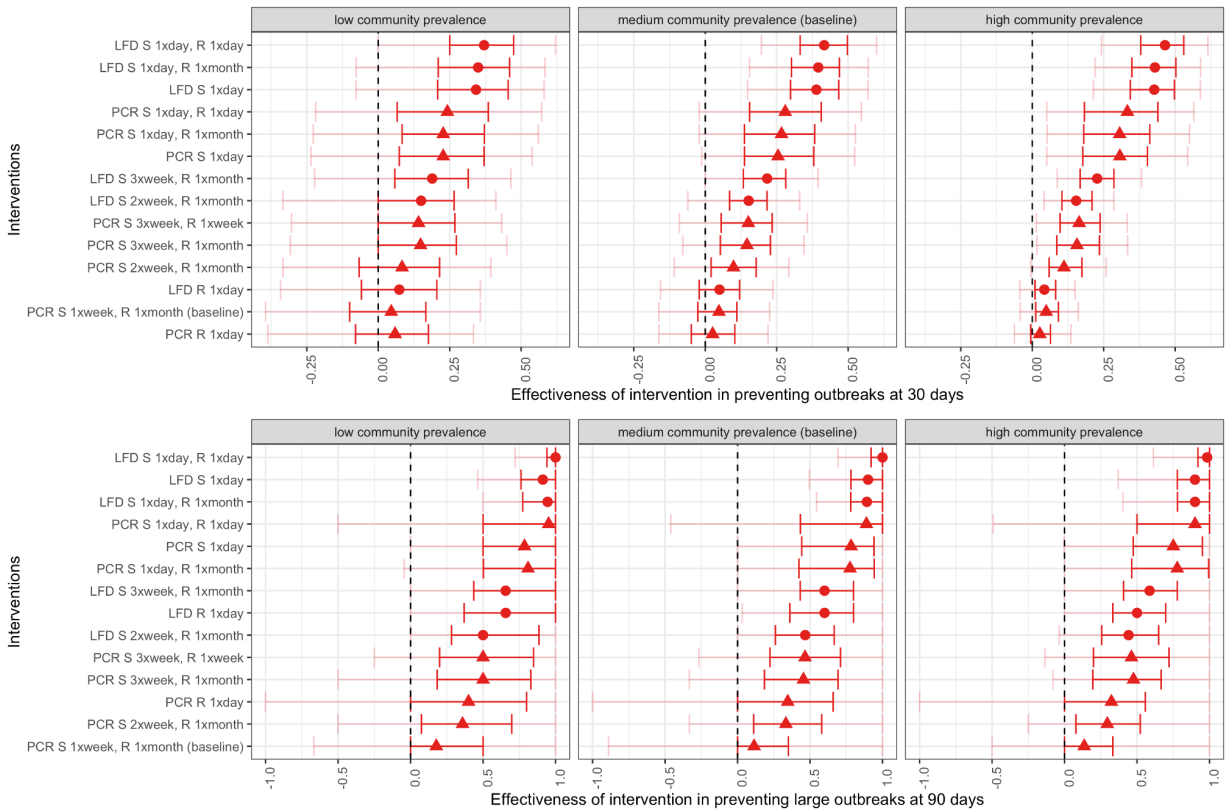


Figure S20. Effectiveness of testing strategies in preventing outbreaks in nursing care homes at 30 days (top panels) and large outbreaks at 90 days (bottom panels) in a scenario where 50% of staff and residents are immune at the start of the simulation, by testing intervention and under low (left panels), medium (baseline, middle panels) and high (right panels) community prevalence. In red, the 25-75%, in pink, the 5-95%. Testing interventions include PCR testing (triangles) and LFD testing (dots). R stands for resident and S for staff.

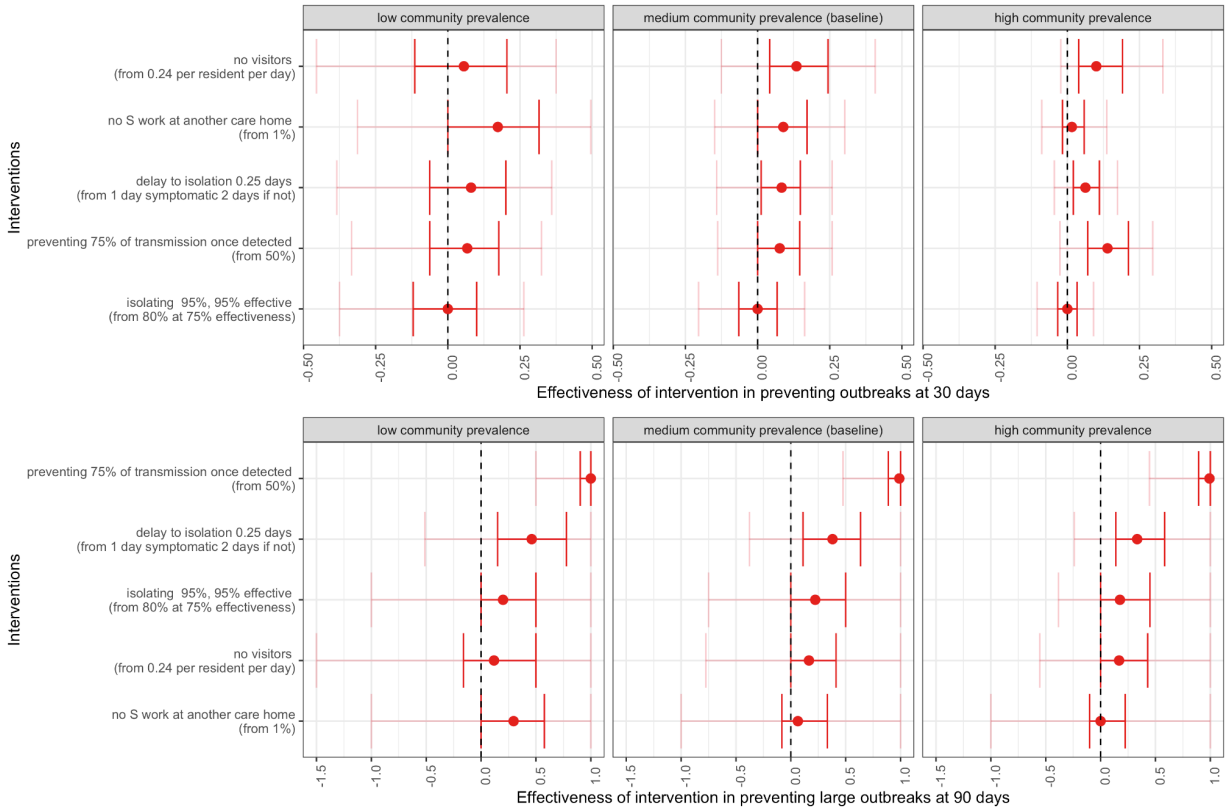


Figure S21. Effectiveness of interventions in preventing outbreaks in nursing care homes at 30 days (top panels) and large outbreaks at 90 days (bottom panels) in a scenario where 50% of staff and residents are immune at the start of the simulation, by low (left panels), medium (baseline, middle panels) and high (right panels) community prevalence. In red, the 25-75%, in pink, the 5-95%. R stands for resident and S for staff.

SUPPLEMENTARY MATERIAL A0

National guidance in England recommends care home providers implement physical distancing, follow shielding guidance, and monitor residents closely for signs of infection (which may be atypical in this population).¹⁸ Residents known to have been exposed to SARS-CoV-2 through contact with a possible or confirmed case of COVID-19 should be isolated or cohorted with other suspected cases where isolation is not possible.¹⁸ Symptomatic residents must be isolated and tested by PCR.¹⁸ Guidance has also been published concerning PPE use for care home staff.¹⁹ Testing upon hospital discharge is required for all care home residents. Since December 2020, upon receipt of a positive test, residents are discharged to “designated settings” (facilities approved by the Care Quality Commission) to isolate for 14 days before returning to their care home.²⁰ Testing has been provided to symptomatic care home residents and staff since the 8th of April 2020, and from the 6th of July 2020 all staff are recommended to be tested weekly and residents every 28 days, independently of their symptom status.²¹ However, delays in the testing pathways have been problematic.²² On the 23rd of December a policy was introduced to test staff twice a week by LFD (in addition to weekly by PCR).²³ Visiting policies in care homes are decided on an individual basis by care home managers.²⁴ In the Vivaldi study, which surveyed 9,081 care homes in England from 26 May to 19 June 2020, 97% of care home managers reported their facilities as having been closed to visitors.²⁵ However, visiting restrictions were eased over the summer of 2020, and lateral flow antigen testing (lateral flow device, LFD) tests are now being used to test all visitors.²¹ LFD tests are point of care tests for SARS-CoV-2 that can display results in 15-30 minutes and have been shown to detect a high proportion of the most infectious individuals.²⁶ However, they have lower sensitivity than laboratory PCR tests for detecting all infections, particularly when carried out by individuals who are insufficiently trained.^{27,28}

SUPPLEMENTARY MATERIAL A1

Stochasticity and sensitivity analyses

Our model was coded in a pomp framework in R using C snippets²⁹ with a time step of one day. The code is available here (public once published):

https://github.com/rmjlr/COVID19_care_home_NPIs.

The model was initialised with all residents being susceptible. The initial proportion of staff in each compartment was informed by results from a dynamic mathematical model of SARS-CoV-2 transmission calibrated to community data⁵.

The stochastic draw determining the number of individuals moving through each transition at each timestep was simulated through Euler-multinomial transitions using the “reulermultinom” function of the pomp package in R.²⁹ Other entries and exits into the care home were modelled using random Poisson processes using the “rpois” function.

We randomly drew 600 parameter sets and, for each, ran 700 simulations for nursing care homes and 800 simulations for residential care homes. The number of parameter sets and simulations per parameter set were determined by examining the point at which the model outputs converged (see Figures S3 and S4).

Univariate sensitivity analyses were carried out to identify the parameters that model outcomes were most sensitive to. We fixed parameter values at the 5th and 95th percentile of their distribution (if the parameter was drawn from a distribution), or selected plausible ranges if they were not, and outputted the probability of an outbreak and of a large outbreak for each parameter value selected.

Natural history of SARS-CoV-2 infection and transmission process

Susceptible residents could become exposed to SARS-CoV-2 through contact with infectious residents and staff in the care home, and through contact with infectious visitors (see below for details). Susceptible staff could become exposed through contact with infectious residents and staff, and through their work in other care homes, and outside of care homes in the community. Exposed residents and staff progressed to either pathway (a), exhibiting preclinical (asymptomatic) infection followed by clinical (symptomatic) infection, or pathway (b), exhibiting asymptomatic infection only.

Infected residents remained in the care home unless hospitalized (described below). Infected staff were removed from the care home if their infection was detected either through testing (described below) or as a result of their symptoms. Staff with asymptomatic infection continued to work until they received a positive test, and otherwise remained infectious within the care home until their recovery. Absent staff were assumed to be absent for a mean duration of 14 days (95% 10.5-17.8) before returning to the care home in a recovered state. Transmission rates were, on average, halved (95% 31-73%) whilst a care home had a detected outbreak (i.e. whilst one or more residents were isolated or one or more members of staff were absent), in order to reflect a step up in IPC measures due to increased awareness of SARS-CoV-2 infection in the care home but a reflection of the difficulty in IPC in this care setting (see $m\beta_d$ in Table S1).

A mean of 80% (95% 72-88%) of absent care home staff were assumed to be replaced by a second pool of staff. The remaining absent staff were not replaced and only resumed work after a mean of 14 days, during which there was a staff vacancy in the care home. When replacement staff became absent they did not return to the care home after their isolation period was completed (since the replacement was temporary). Replacement staff exited the care home at the same rate that the original staff members recovered and re-entered the care home. Original and replacement staff were considered to be the same in relation to force of infection calculations, except replacement staff were more likely to work at more than one care home and hence have a higher probability of being infected (details below).

Residents

Susceptible residents could become exposed to SARS-CoV-2 through contact with infectious residents (λ_{r2r}) and staff (λ_{s2r}) in the care home, and through contact with infectious visitors (λ_{v2r}) (see Supplementary material A1 for details). Susceptible staff could become exposed through contact with infectious residents (λ_{r2s}) and staff (λ_{s2s}), and through their work in other care homes (λ_{o2s}), and outside of care homes in the community (λ_{c2s}).

Exposed residents progressed to either pathway (a), exhibiting preclinical (asymptomatic) infection followed by clinical (symptomatic) infection, or pathway (b), exhibiting asymptomatic infection only. Exposed residents progressed to pathways (a) and (b) at proportions $1-p_a$ and p_a , respectively, after a latent period $1/\epsilon$. Infected pre-clinical residents progressed to clinical infection at rate τ (symptom onset). Clinical infection was further subdivided into two periods: early clinical infection with high infectiousness followed by late clinical infection with low infectiousness, each having the same duration ($1/\omega$ and $1/\phi$). This enabled better characterisation of viral load peaking at symptom onset and decreasing rapidly thereafter^{2,3}. Residents recovered from infection at a recovery rate ϕ and were considered immune from future SARS-CoV-2 infection for the duration of the simulation. The duration of asymptomatic infection $1/\phi_a$ (pathway (b)) was assumed to equal the duration of the combined preclinical and clinical duration $1/\tau + 1/\omega + 1/\phi$ (pathway (a)).

Transmissibility of SARS-CoV-2 was assumed to vary over the different stages of pathway (a) (pre-clinical, early clinical, and late clinical stages). Conversely, for pathway (b), transmissibility was assumed to remain at the same rate over the full duration of infectiousness.

The overall force of infection between residents λ_{r2r} was calculated as follows (simplified, see full equation below):

$$\lambda_{r2r} = \beta_{pc} \frac{I_{pc}}{N_r} + \beta_{ch} \frac{I_{ch}}{N_r} + \beta_{cl} \frac{I_{cl}}{N_r} + \beta_a \frac{I_a}{N_r}$$

where I_{pc} represents the number of residents in the infectious pre-clinical compartment, I_{ch} is the number of residents in the infectious clinical with high infectiousness compartment, I_{cl} is the number of residents in the infectious clinical with low infectiousness compartment, I_a is the number of residents in the infectious asymptomatic compartment, and N_r represents the total number of residents present in the care home. Among individuals in pathway (a) ie. those who eventually present with symptoms (individuals go through pre-clinical, early clinical, and late

clinical stages), the transmission rate was subdivided into β_{pc} for preclinical SARS-CoV-2 infection, β_{ch} for early clinical infection and β_{cl} for later clinical infection. For pathway (a), we assumed a total reproduction number $R0_a$ ($R0$ for pathway (a)) over the full infectious period. The total duration of infectiousness was subdivided into a preclinical infection period, a period of clinical symptomatic infection with high levels of infectiousness and a period of clinical symptomatic infection with low levels of infectiousness. Assuming that on average that a proportion $p_{transmission_pc_vs_c}$ of transmission occurs during preclinical infection compared to clinical infection and that a proportion $p_{transmission_cl_vs_ch}$ of transmission occurs in the later stage of clinical infection compared to the early stage of clinical infection, we find:

$$\beta_{pc} = \frac{R0_a \times p_{transmission_pc_vs_c}}{d_{preclinical_infection}};$$

$$\beta_{ch} = \frac{R0_a \times (1 - p_{transmission_pc_vs_c}) \times (1 - p_{transmission_cl_vs_ch})}{d_{clinical_infection_h}};$$

$$\beta_{cl} = \frac{R0_a \times (1 - p_{transmission_pc_vs_c}) \times p_{transmission_cl_vs_ch}}{d_{clinical_infection_l}}.$$

A separate transmission rate was estimated for pathway (b), where residents remain asymptomatic during the full duration of their infection. This transmission rate was derived assuming $R0_b$ over the full asymptomatic infectious period:

$$\beta_a = \frac{R0_b}{d_{total_infectiousness}},$$

where $R0_b = R0_a \times m_{R0_b}$ and $0 < m_{R0_b} < 1$.

The full equation for the force of infection between residents λ_{r2r} is as follows:

$$\lambda_{r2r} = \beta_{pc} \frac{I_{pc} + I_{pcpi} + (I_{pci} \times m_i)}{N_r} + \beta_{ch} \frac{I_{ch} + I_{chpi} + (I_{chi} \times m_i)}{N_r} + \beta_{cl} \frac{I_{cl} + I_{clpi} + (I_{cli} \times m_i)}{N_r} + \beta_a \frac{I_a + I_{api} + (I_{ai} \times m_i)}{N_r},$$

where β_{pc} was the transmission rate for those infectious pre-clinical, I_{pc} was the number of residents infectious pre-clinical that would not be isolated, I_{pcpi} was the number of residents

infectious pre-clinical that would be but were not yet isolated, I_{pci} was the number of residents infectious pre-clinical isolated, m_i was the relative infectiousness of residents isolated compared to those that were not, N_r was the number of residents in the care home, β_{ch} was the transmission rate for those highly infectious presenting with clinical symptoms, I_{ch} was the number of residents highly infectious presenting with clinical symptoms that would not be isolated, I_{chpi} was the number of residents highly infectious presenting with clinical symptoms that would be but were not yet isolated, I_{chi} was the number of residents highly infectious presenting with clinical symptoms that were isolated, β_{cl} was the transmission rate for those less infectious presenting with clinical symptoms, I_{cl} was the number of residents less infectious presenting with clinical symptoms that would not be isolated, I_{clpi} was the number of residents less infectious presenting with clinical symptoms that would be but were not yet isolated, I_{cli} was the number of residents less infectious presenting with clinical symptoms isolated, β_a was the transmission rate for those asymptomatic, I_a was the number of asymptomatic residents that would not be isolated, I_{api} was the number of asymptomatic residents that would be but were not yet isolated, I_{ai} was the number of asymptomatic residents isolated.

In the baseline scenario, residents could become exposed to infection through contact with other (infectious) residents or staff. Therefore, the total rate of exposure of residents λ_R was defined as:

$$\lambda_R = \lambda_{r2r} + \lambda_{s2r} + \lambda_{v2r},$$

where λ_{r2r} describes the force of infection from residents to residents (described above), λ_{v2r} described the force of infection from visitors to residents (described below), and λ_{s2r} describes the force of infection from staff to residents, calculated as follows (simplified, see full equation below):

$$\lambda_{s2r} = \beta_{pc} \frac{I_{pcs}}{N_s} + \beta_{ch} \frac{I_{chpis}}{N_s} + \beta_a \frac{I_{as}}{N_s},$$

where the transmission rates are calculated as described above for λ_{r2r} and N_s describes the total number of staff in the care home, including replacement staff. I_{pcs} were staff in the infectious pre-clinical compartment, I_{as} were staff in the infectious asymptomatic compartment, and I_{chpis} describes symptomatic and highly infectious staff who were present in the care home before becoming absent after a delay $1/\gamma_c$.

The full equation for the force of infection from staff to residents λ_{s2r} is as follows:

$$\lambda_{s2r} = \beta_{pc} \frac{I_{pcs} + I_{pcpis} + I_{pcs2} + I_{pcpis2}}{N_s} + \beta_{ch} \frac{I_{chpis} + I_{chpis2}}{N_s} + \beta_a \frac{I_{as} + I_{apis} + I_{as2} + I_{apis2}}{N_s},$$

where β_{pc} was the transmission rate for those infectious pre-clinical, I_{pcs} was the number of original staff infectious pre-clinical that would not be absent, I_{pcpis} was the number of original staff infectious pre-clinical that would be but were not yet absent, I_{pcs2} was the number of

replacement staff infectious pre-clinical that would not be absent, I_{pcpis2} was the number of replacement staff infectious pre-clinical that would be but were not yet absent, N_s was the number of staff in the care home, β_{ch} was the transmission rate for those highly infectious presenting with clinical symptoms, I_{chpis} was the number of original staff highly infectious presenting with clinical symptoms that would be but were not yet absent, I_{chpis2} was the number of replacement staff highly infectious presenting with clinical symptoms that would be but were not yet absent, β_a was the transmission rate for those asymptomatic, I_a was the number of asymptomatic original staff that would not be absent, I_{apis} was the number of asymptomatic original staff that would be but were not yet absent, I_{as2} was the number of asymptomatic replacement staff that would not be absent, I_{apis2} was the number of asymptomatic replacement staff that would be but were not yet absent.

Staff

Staff could become infected through contact with residents, through contact with other staff, through their work in other care homes, or outside of care homes (in the community). Therefore, the total rate of exposure of staff λ_s was defined as:

$$\lambda_s = \lambda_{r2s} + \lambda_{s2s} + \lambda_{c2s} + \lambda_{o2s},$$

where λ_{r2s} represents the force of infection from residents to staff, which was assumed to be equal to the force of infection from residents to residents λ_{r2r} (described above); λ_{s2s} describes the force of infection from staff to staff, assumed to be equal to the force of infection from staff to residents λ_{s2r} (described above); λ_{c2s} was the force of infection from the community to staff and λ_{o2s} describes the force of infection to staff from their work in other care homes. λ_{c2s} was calculated as follows:

$$\lambda_{c2s} = \frac{R_c}{d_{total_infectiousness_C}} \times p_{C_infectious},$$

where R_c was the reproduction number in the community, assumed in the baseline scenario (medium community prevalence) to follow a Gamma distribution of mean 1, and $d_{total_infectiousness_C}$ was the duration of infectiousness in the community, assumed to follow a Gamma distribution of mean of 5 days⁴. The probability of an individual in the community being infectious ($p_{C_infectious}$) was derived from a dynamic mathematical model of infection calibrated to community data⁴ and the same distribution was throughout our simulations for that specific scenario (varied for the low and high community prevalence scenarios).

On average 1% of original staff were assumed to work in another care home (pers. comm. lead of care home survey Thames Valley, Dr Conall Watson, June 2020). On average, we assumed 20% of replacement care home staff worked at another care home. The force of infection to staff working in another care home, λ_{o2s} , was calculated as:

$$\lambda_{o2s} = (\lambda_{or2s} + \lambda_{os2s}) = [\beta_{pathway a} \times p_{res infectious pathway a} + \beta_{pathway b} \times p_{res infectious pathway b}] + \dots$$

$$\dots + [\beta_{pathway a} \times p_{staff infectious pathway a} + \beta_{pathway b} \times p_{staff infectious pathway b}]$$

where $\beta_{pathway a}$ and $\beta_{pathway b}$ were defined as:

$$\beta_{pathway a} = \frac{R0_a}{d_{total infectiousness}}, \beta_{pathway b} = \frac{R0_b}{d_{total infectiousness}},$$

and $p_{res infectious pathway a}$ and $p_{res infectious pathway b}$ were the probability of a resident being infectious in pathway (a) and pathway (b), respectively, and $p_{staff infectious pathway a}$ and $p_{staff infectious pathway b}$ were the probability of a staff member being infectious in pathway (a) and pathway (b), respectively.

We make the following assumptions regarding the probability of residents and staff being on different infectious pathways:

$$p_{res infectious pathway a} = p_{care home outbreak} \times p_{res inf} \times (1 - p_a),$$

$$p_{res infectious pathway b} = p_{care home outbreak} \times p_{res inf} \times p_a,$$

$$p_{staff infectious pathway a} = p_{staff infectious pathway b} = p_{care home outbreak} \times p_{staff inf} \times p_{as},$$

where $p_{care home outbreak}$ was the probability of another care home has an outbreak on a given day, $p_{res inf}$ is the probability that a resident in a care home with an outbreak is infectious, $p_{staff inf}$ is the probability that a staff member in a care home with an outbreak is infectious, p_a is the probability that a resident follows pathway (a), and p_{as} is the probability that a staff member follows pathway (a).

In the baseline scenario (medium community prevalence), we assumed that the mean probability of a care home having an outbreak on any given day was 25% (corresponding to ~4,000 out of ~15,000 care homes having an outbreak), and the mean probability of a resident (or staff member) being infectious within a care home with an outbreak was 10%, corresponding approximately to 3 residents or staff in a care home being infectious in an average sized residential care home. As denoted above, 50% of staff and 40% of residents were assumed to never present with symptoms (i.e. to be in pathway (b)).

The proportion of replacement staff entering each infection state compartment was assumed to be the same as the proportion of the general community in each disease compartment, and informed by a dynamic mathematical model of infection calibrated to community data⁵.

Visitors

In the scenarios including visitors, residents could additionally become exposed through contact with visitors:

$$\lambda_{v2r} = \beta_a \frac{N_{visitors}}{N_r}$$

The transmission rate for asymptomatic infection (β_a) was also used for visitors, thus we assumed that any infected visitors were asymptomatic if permitted entry into the care home (for simplicity, we did not allow visitors to be in the preclinical stage of COVID-19 infection). The number of infected visitors per day in the care home, $N_{visitors}$, was given by:

$$N_{visitors} = n_v \times N_r \times p_{v_{infectious}},$$

where n_v was the expected number of visitors per resident per day, and $p_{v_{infectious}}$ represents the probability of a visitor being infectious, which we assumed was the same as the probability of being infectious without symptoms in the community overall, and was parameterised using a SARS-CoV-2 transmission model calibrated to community data³⁰. Staff were assumed not to become exposed through contact with visitors.

SUPPLEMENTARY MATERIAL A2

Mortality and hospitalisation dynamics

Residents were assumed to exit the care home either due to hospitalisation (either for COVID-19 or other reasons) or death. Residents entered the facility exclusively from hospital (it was assumed that during the COVID-19 pandemic, community admissions of residents to care homes were rare). We also assumed that the proportion of residents leaving the care home to return to the community or transfer to another care home was negligible. Residents without symptomatic COVID-19 (i.e. those in the S , E , I_{pc} , I_a and R compartments) were assumed to be hospitalised at background rate κ and die at background rate δ , and residents presenting with COVID-19 symptoms (i.e. those in the I_{ch} , I_{cl} compartments) were assumed to be hospitalised at rate κ_c and die at rate δ_c (see below for details).

Non-COVID-19 care home exit and entry processes were modelled stochastically as Poisson processes with identical rates. Therefore, without COVID-19, the care home was full at all times (100% occupancy). Non-COVID-19 care home exits (ie. background hospitalisation and mortality from compartments S , E , I_{pc} , I_a , R) were immediately replaced with entries to the care home from hospital. These entries included both residents returning from a hospital visit that was unrelated to COVID-19, and residents newly admitted to the care home from hospital. When COVID-19 symptomatic residents were present in the care home (I_{ch} , I_{cl}), their deaths were not replaced with new care home admissions from hospitals, as COVID-19 deaths occurred at a faster rate than replacement of residents, decreasing care home occupancy rates during the outbreak. Residents could die from COVID-19 both in the care home or in the hospital.

In the baseline scenario (medium community prevalence scenario), a mean of 5% of residents entering the care home from hospital were assumed to be recovered from SARS-CoV-2 infection all of whom entered the recovered (R) compartment, 0.07% residents entering the care home were assumed to be infected (of which 69% were exposed (E), 13% infectious pre-clinical (I_{pc}), 18% asymptomatic (I_a)). This was derived from combining the outputs of two mathematical models fit to English data from the community and to hospital data^{15,30} (see Table S1 for details). The remaining residents entered the care home susceptible (S). We assumed that no residents who were hospitalised for reasons unrelated to COVID-19 entered the care home from hospital presenting with COVID-19 symptoms (I_{ch} , I_{cl} compartments).

Residents hospitalised for COVID-19 returned to the care home with a probability $p_{survival}$ (the probability that they survived their hospitalisation). In these simulations, therefore, the care home occupancy was further reduced due to COVID-19 deaths within the hospital. In the baseline scenario, on average 94% of residents who were admitted to hospital due to COVID-19 complications (I_{ch} , I_{cl}) and who survived their hospital stay were assumed to be fully recovered upon their return to the care home (direct re-entry to the R compartment). The remaining residents (on average 6%) were assumed to have a low level of infectiousness upon their return to the care home and were isolated upon re-entry. This assumption reflects that the tail of the viral load distribution beyond the average duration of hospital stays for COVID-19.²⁻⁴

Rates of hospitalisation and mortality have varied substantially during the pandemic.³¹ Prior to the COVID-19 pandemic, nursing care home residents required but also received greater care, resulting in lower background rates of hospitalisation (κ) in nursing care homes than in

residential care homes (0.84 vs. 1.13 per person per year in 2016/17³²). Policy changes and changes in the perception of risk of hospitalisation have resulted in a decrease of the non-COVID hospitalisation rate for care home residents during the COVID-19 pandemic, particularly in those living in residential facilities.³¹ In the baseline scenario (medium community prevalence), the rates of hospitalisation were 0.5 hospital visits per person per year for both types of facility, as extracted from SUS data (see below for details). The background mortality rate (δ) was higher in nursing than in residential care homes (mean 0.4 vs. 0.2 per person per year, calculated using the number of non-COVID deaths in care homes published by the ONS³³, adjusted using estimates of lengths of stay prior to the COVID-19 pandemic from the literature, by type of facility³⁴, see below).

Not all care home residents with COVID-19 symptoms are hospitalised. The COVID-19 symptomatic hospitalisation rate (κ_c) was calculated by dividing the proportion of care home residents with COVID-19 who were hospitalised (mean 17%) by the duration of symptomatic infectiousness (mean five days) (for further details, see below). The hospitalisation rate for residents with COVID-19 clinical infection was assumed to be the same in residential and nursing care homes, as it was not evident that this rate would differ between settings. The COVID-19 symptomatic death rate δ_c was informed by an assumed mean case-fatality ratio of 25% (CFR literature estimates from care home residents range from 17%-36%^{6-9,12,13}) for nursing care homes, and an assumed mean of 80% of these deaths occurring within the care home (20% of these deaths occurred during hospital visits, see below)¹⁴.

Hospitalisation rate for non-COVID-19 (κ)

Weekly hospital admission rates from residential care homes and nursing homes from the week commencing 20 January to the week commencing 15 June 2020 were calculated using pseudonymised administrative data on hospital admissions from the Secondary Uses Service (SUS) database³⁵. Care home residents were identified in SUS through linkage to address information from the National Health Applications and Infrastructure Services (NHAIS) database, which was matched to addresses of care homes registered with the Care Quality Commission (CQC), using validated linkage methodology. Elective and emergency hospital admissions to National Health Service (NHS) hospital trusts in England were included for individuals who had an address match to a care home in January 2020 and were still living in a care home at the time of admission. Hospital admissions were excluded if the administrative category was recorded as private patient, if the admission method was a transfer or was missing or if the patient classification for elective admissions was not recorded as day case or ordinary admission. To calculate hospital admission rates, admissions were also excluded if the primary diagnosis was suspected or confirmed COVID-19 (ICD-10 codes U07.1 and U07.2). Weekly admission rates per resident were calculated by across all residents for admissions from the week commencing 20 January to the week commencing 15 June 2020, controlling for the number of days spent in care homes across all residents. All processing of address information, and subsequent linkage of patient information, was carried out by the National Commissioning Data Repository (NCDR) and all data were anonymised in line with the Information Commissioner's Office (ICO)'s code of practice on anonymisation.

Death rate from non-COVID-19 causes (δ)

Care home resident deaths that were not due to COVID-19 (obtained by subtracting COVID-19 deaths from all-cause deaths) occurring within care homes, were extracted from the latest published ONS report, which reported deaths occurring until the 12 June 2020.³³ 7,378

non-COVID-19 deaths of care home residents occurring in care homes were reported for the period of the 14 May 2020 to the 12 June 2020 (the last 30 days of data available).

Assuming an occupancy of 80%, and that 11% of residents had COVID-19²⁵, the denominator population for the death rate was calculated as follows:

$$N \text{ residents without COVID} = (N \text{ beds registered} \times \text{occupancy}) - (0.11 \times (N \text{ beds registered} \times \text{occupancy})) \\ = 460,000 * 0.8 - 0.11 * 460,000 * 0.8 = 327,520.$$

The mean non-COVID-19 death rate, $\mu(\delta)$, was therefore given by:

$$\mu(\delta) = 7,378 / (30 * 327,520) = 0.00075 \text{ per person per day, or } 0.3 \text{ per year}$$

Prior to the pandemic, the death rate in nursing care homes was higher than for residential care homes. Steventon et al. reported a length of stay in care homes of 283 for nursing care homes and 544.5 for residential care homes; and that 55% of nursing care home residents died within 30 days of leaving the facility, and 50% for residential care homes. Therefore, the mean pre-pandemic rates for nursing and residential care homes ($\mu(\delta_{pn})$ and $\mu(\delta_{pr})$, respectively) were given by:

$$\mu(\delta_{pn}) = (1/283) * 0.55 = 0.002 \text{ per person per day, or } 0.7 \text{ per year}$$

$$\mu(\delta_{pr}) = (1/544.5) * 0.5 = 0.0009 \text{ per person per day, or } 0.3 \text{ per year.}$$

$$\mu(m_{\delta_{rvn}}) = \frac{\mu(\delta_{pr})}{\mu(\delta_{pn})}$$

These mortality rates were similar to those reported by Shah et al. in 2013.³⁶

The CQC register shows that approximately 50% of care homes were residential and 50% nursing.³⁷ Therefore, we adjusted the May/June death rates to give rates specific to nursing (δ_n) and residential (δ_r) care homes:

$$\mu(\delta_n) = \frac{\mu(\delta)}{0.5 \times \mu(m_{\delta_{rvn}}) + 0.5} = \frac{0.00075}{0.5 \times \frac{0.0009}{0.002} + 0.5} = 0.001 \text{ per day or } 0.4 \text{ per year}$$

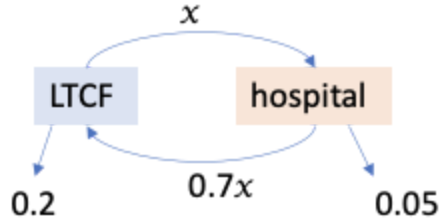
$$\mu(\delta_r) = \mu(\delta) \times \mu(m_{\delta_{rvn}}) = 0.0005 \text{ per day or } 0.2 \text{ per year}$$

COVID-19 symptomatic hospitalisation rate (κ)

CFR literature estimates from care home residents range from 17%-36%^{6-9,12,13}. For the purpose of this analysis we assumed a mean CFR of 25%. During the period of the 14th of May 2020 to the 12th of June 2020 (the last 30 days of data available, see above), approximately 80% of residents deaths occurred within the care home, and 20% in hospitals.¹⁴ Therefore, we assumed that, on average, $0.25 \times 0.2 = 0.05$, 5% of COVID-19 residents died in hospital.

COVID-19 hospital mortality rates were calculated from SUS data for care home residents admitted between 18 May 2020 and 14 June 2020, using the destination on discharge variable. These data show a mean of 30% of patients admitted to hospital for COVID-19 died in hospital during the this period ($1 - p_{\text{survival}}$).

We calculated the mean probability of a resident with COVID-19 (symptomatic) being hospitalised from these data. We can illustrate the problem as follows:



Where x was the the mean probability of a resident with COVID-19 (symptomatic) being hospitalised and, on average, $p(\text{resident with COVID} - 19 \text{ dying in hospital}) = 0.05 = (1 - 0.7)x$

Therefore,

$$x = \frac{p(\text{resident with COVID-19 dying in hospital})}{1 - p_{\text{survival}}} = \frac{0.05}{0.3} = 0.17$$

The COVID-19 symptomatic hospitalisation rate κ_c was then calculated by dividing the proportion of care home residents with COVID-19 hospitalised (Beta distribution with a mean of 17%) by the duration of clinical infectionness (Gamma distribution with mean of 5 days).

COVID-19 symptomatic death rate (δ_c)

The COVID-19 symptomatic death rate in nursing care homes ($\delta_{c,n}$) was calculated as follows:

$$\delta_{c,n} = \frac{CFR \times p_{\text{death res within care home}}}{\text{duration of clinical infectiousness}}$$

As most of the CFR studies were based in nursing care homes, this death rate was attributed to nursing care homes. The death rate for symptomatic residents in residential care homes ($\delta_{c,r}$) was calculated by adjusting this rate by the pre-pandemic ratio of the background mortality in nursing care home vs. residential care homes as follows:

$$\delta_{c,r} = \delta_{c,n} \times m_{\delta_{rvn}}$$

SUPPLEMENTARY MATERIAL A3

Three community prevalence scenarios were considered: low, medium (baseline scenario), and high.

The community prevalence was derived from an established transmission model fit to community data³⁰. We extracted the proportion of individuals in all ages that were susceptible (S), exposed (E), infectious preclinical (Ipc), infectious asymptomatic (Ia) and recovered (R) on the 2020-07-15 (low prevalence scenario), 2020-09-30 (medium prevalence scenario), and 2020-04-01. These were used to inform:

- the force of infection from visitors to residents (λ_{v2r} , through the probability that a visitor is infectious $p_{v_{infectious}}$, see Supplementary material A1),
- the force of infection from the community to staff (λ_{c2s} , through the probability of an individual in the community being infectious $p_{C_{infectious}}$),
- the proportion of replacement staff in each infectious state ($p_{S s2}, p_{E s2}, p_{E, EI s2}, p_{Ipc, EI s2}, p_{Ia, EI s2}, p_{R s2}$), and
- the proportion of staff starting the simulation susceptible (S) and recovered (R).

We extracted the proportion of individuals aged over 70 that were susceptible (S), exposed (E), infectious preclinical (Ipc), infectious asymptomatic (Ia) and recovered (R) on the 2020-07-15 (low prevalence scenario), 2020-09-30 (medium prevalence scenario), and 2020-04-01. These were used to inform:

- The relative proportion of susceptible to recovered residents entering the care home from hospital after a hospitalisation unrelated to COVID-19.

The hospital discharge prevalence for those aged 65+ was derived from an established transmission model fit to hospital data¹⁵. We extracted the proportion of individuals that were susceptible (S), exposed (E), infectious preclinical (Ipc), infectious asymptomatic (Ia) and recovered (R) on the 2020-07-15 (low prevalence scenario), 2020-05-01 (medium prevalence scenario), and 2020-04-01. The early May hospital discharge data was used as a proxy for late September since the model output data was only available until mid-July (in early May the community prevalence was at a similar level as in late September). These data were used to inform:

- the proportion of residents entering each infectious state from hospital after a non-COVID-19 hospitalisation ($p_{S s2}, p_{E s2}, p_{E, EI s2}, p_{Ipc, EI s2}, p_{Ia, EI s2}, p_{R s2}$).

The latest data point for the non-COVID-19 hospitalisation rate κ available from SUS was for the week starting on 15 June (see Supplementary material A2 above). The adjusted emergency admissions for the overall population increased by 8% from June to July and by 11% from June to October (publicly available adjusted monthly NHSE data³⁸). Assuming the same rate of increase in non-COVID-19-hospitalisation rates for care home residents, we adjusted the rate of the week starting the 15 June using the NHSE data to approximate the hospitalisation rate in mid-July (low community prevalence scenario) and late September (medium community prevalence scenario). The non-COVID-19 hospitalisation rate for residents in the high community prevalence scenario was extracted directly from SUS (see Supplementary material

A2 above) for the week starting on the 30 March. The late September approximation bore similar results to the SUS data for early May.

The reproduction number in the community R_c was assumed to be 0.8 in the low community prevalence scenario, 1 in the medium community prevalence scenario, and 1.5 in the high community prevalence scenario. These were used to calculate the force of infection from the community to staff λ_{c2s} (see Supplementary material A1 above for further details).

We also assumed that the probability of a care home experiencing an outbreak $p_{care\ home\ outbreak}$ would differ by community prevalence scenario. The $p_{care\ home\ outbreak}$ is used to calculate the force of infection to staff working in another care home λ_{o2s} . In the low community prevalence scenario we assumed 10% of care homes had an outbreak, in the medium community prevalence scenario we assumed 25% of care homes had an outbreak, and in the high community prevalence scenario we assumed 40% of care homes had an outbreak.

All other parameters were kept the same through the three community prevalence scenarios.

SUPPLEMENTARY MATERIAL A4

The impact of each strategy was assessed by estimating the cumulative probability of an outbreak (proportion of simulations with 1 or more infectious symptomatic residents in the care home), and of a large outbreak (proportion of simulations with 10 or more infectious symptomatic residents in the care home) over time. Eventually, every simulation resulted in an outbreak, therefore, we chose to compare the effectiveness of IPC interventions at two cut-offs: 30 days for the probability of an outbreak and 90 days for a large outbreak. Beyond 90 days it was unreasonable to assume the community prevalence scenario remained unchanged. The effectiveness of an intervention (i.e. the relative reduction in the probability of an outbreak) in preventing outbreaks at 30 days was calculated as follows:

Effectiveness of intervention in preventing an outbreak at 30 days =

$$1 - \frac{\text{cumulative probability of an outbreak at 30 days under intervention}}{\text{cumulative probability of an outbreak at 30 days under no intervention}}$$

When assessing the effectiveness of testing, the comparison “no intervention” scenario referred to no testing, whilst it referred to the baseline assumptions when assessing the effectiveness of IPC interventions. Parameter sets were matched to enable the direct intervention comparison. The effectiveness of an intervention in preventing large outbreaks at 90 days was calculated in the same way. Approximately 3% of parameter sets yielded no large outbreaks at 90 days, and were discarded to enable the calculation of effectiveness.

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